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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                 Result
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Maximum DB seq
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
                                                                                                                                                                                                                    and is derived by analysis of the total score distribution.
  484.2
460.8
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1: en,
2: em,
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  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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1807
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  BE053804
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BC013141 Homo sapi
BH600970 BCGCN27TR
BE55887 T W_CED002
BI118849 EST237 Di
BG594704 EST493882
W43397 22774 CD4-1
A1994124 701499210
AL518877 AL518877
BG368908 HYSME1002
BE053804 GA_EA003
AL531607 AL531607
AW396525 sh28h04 y
AW308961 sf92d04 y
AW308961 sf92d04 y
AL558916 BB611086
BB611086 BB611086
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45	44	43	42	41	40	39	38	37	36	35	4	(L)	32	1	30	29	28	27	26	25	24	23	22	21	20	19	18
342.2	342.2	343.2	343.2	344.8	345	346	347	349.2	352.8	353.2	353.8	360	361	363.4	365.2	369.6	372	372	372.8	373.4	374.2	374.8	377.2	377.6	78	78	380.6
18.9	18.9	19.0	19.0	19.1	19.1	19.1	19.2	19.3		19.5	19.6							20.6				20.7				21.0	21.1
878	643	871	722	528	345	603	890	650	1034	866	910	737	636	910	765	637	1007	905	977	882	988	898	437	696	986	613	1030
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BF631408	AW616696	BE747628	BG914796	A1736699	AV536771	BE517647	AL527966	BG598526	BM461585	AL555361	AL546378	BI177518	BI075248	BG756668	AJ394397	AW686294	BM452740	BI855025	CNS072YS	BG367319	BM468325	AL541430	R90034	BG597901	AL536160	BG521741	CNS06MLI
BF631408 HVSMEb001	AW616696 EST323107	BE747628 601577573	BG914796 602813602	A1736699 sb32d06.y		BE517647 WHE0801_F		BG598526 EST503426	BM461585 AGENCOURT	AL555361 AL555361		BI177518 EST518463	в1075248 IP1_17_н0	BG756668 602715527	AJ394397 AJ394397	AW686294 NF036C08N	BM452740 AGENCOURT	BI855025 603382030	AL426842 clone BAO	BG367319 HVSMEi001		AL541430 AL541430	R90034 16389 Lambd	BG597901 EST496579	AL53616	13-	AL405628 T3 end of

## ALIGNMENTS

FEATURES			REMARK COMMENT	JOURNAL .	REFERENCE AUTHORS	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: d Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557640 This clone has the following problem: incomplete processing.	Sequencing center Center code: BCM-HGSC Center code: BCM-HGSC.bcm.tmc.edu/cdna/ Centact: villalon@bcm.tmc.edu. Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W., Muzny,D.M., Gibbs,R.A.	Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome	oba NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk	Direct Submission Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 1627)  Strausberg,R.	BC013141 1627 bp mRNA linear HTC 29-AUG-2001 Homo sapiens, clone IMAGE:4475960, mRNA. BC013141 BC013141 GI:15341911

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BASE COUNT
ORIGIN
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978 aggttgcttcaatctttcaatcaaaggtcatgctgagtgcgtcaaatttatgagatcgtt
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                                                                                                                              960 TATAGATGATGAGTCATATGGGCAGATATTTAAGCCTATTATCTCAAAGGTGATGGAGAT
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/db_xref-"taxon:9606"
/clome-"IMAGE:4475960"
/tissue_type-"Prostate, adenocarcinoma
/clone_lib-"NIH_MGC_91"
/lab_host-"DH10B"
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Pred. No. 2e-117;
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Query Match
Best Local S
Matches 551
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TITLE
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1 (bases 1 to 774)
1 (chases 1 to 774)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Other_GSSs: BOGCN27TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                         primer: TR
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                                                                                                      /db_xref-*taxon:3712"
/dlone="BOGCN27"
/clone="BOGCN27"
/clone="yebc="bocs: site_1: Bstx1; 2-3 kb sheared /note="vector: pHOS1; Site_1: Bstx1; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
a 194 c 174 g 184 t
                                                                                                                                                                                                                            /organism="Brassica oleracea"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                 26.88;
               Score 484.2; DB 12; Pred. No. 5.2e-112;
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VERSION
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                Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, US Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                          1 (bases 1 to 819)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
                                                                                                                                                           Contact: Wing RA
                                                                                                                                                                                  Unpublished (2001)
                                                                                                                                                                                                           for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf CDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE558877 819 bp mRNA linear EST 23-OCT-2001
HY_CEDD0020K09f Hordeum vulgare seedling green leaf EST library
HYCDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HY_CED0020K09f, mRNA sequence.
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare
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                         ACATCGCCATCAACTGGTCAGGGGGCCTGCACCATGCTAAGAAGTGCGAGGCCTCAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total hq bases = 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close), Phagemids swere plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing), Plasmid DNA perparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kileinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)*
a 239 c 216 g 191 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="seedling green leaf"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library HVcDNA0005 (Blumeria challenged)"
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/clone_lib-"Hordeum vulgare seedling green leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="CI16151 (M
/db_xref="taxon:4513"
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/cultivar="CI16151 (Mla6)"
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74.9%;
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Pred. No. 4.7e-106;
0; Mismatches 202;
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BI118849
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EST.
                                                                                                                                                      BTH-downregulated
Insert Length: 917 Std Error: 0.00
Seq primer: M13 Forward and reverse.
Location/Qualifiers
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EST237 Differentially expressed cDNA libraries of BTH-treated/blast
fungus-infected rice leaf tissues Oryza sativa cDNA clone HNBN-w14,
                                                                                                                                                                                                                                                                                                   Department of Plant Pathology
University of Wisconsin-Madison
Rm 689, Russell Laboratories, 16
                                                                                                                                                                                                                                                                                                                                                                   Song, F.M. and Goodman, R.M.
Molecular cloning of differentially expressed
systemic acquired resistance in rice
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                        Contact: Song, F.M.; Goodman, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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Oryza sativa
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/clone="HNBN-w14"
/clone_lib-"Differentially expressed cDNA libraries |
BTH-treated/blast fungus-infected rice leaf tissues"
/tissue_type-"Seedling leaves"
                                                                                     /cultivar="Yuanfengzao (a susceptible variety blast disease)"
                                                                      /db_xref="taxon:4530"
                                                                                                                         /organism="Oryza sativa"
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Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seg primer: M13F-R.
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Solanum tuberosum
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1 (bases 1 to 760)
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
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/cultivar-"Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
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/clone="cSTS12024"
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Pred. No. 1.4e-97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potato.
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG594704
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 749)
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                                                                                                                                                                                                                                                                                                                                       Division tel 1-800-711-6195, email cdna@resgen.com
Seg primer: M13F-R.
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                                     /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                 tubers
                                                                                                                                                                                                                       /organism="Solanum tuberosum"
/Cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS8A2"
                                                                                                                                               /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
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               o
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Local Similarity 76.0%;
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                                 l (bases 1 to 535)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
                                                                                     Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                          thale cress.
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             E. and Somerville,C
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Pred. No. 1.8e-96;
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Michigan State University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lansing, Mi
Tel: 517-353-0854
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                                                                                                                                                                                                  127
                                                                                                                                                                                                                                                                                                                                                                             reaction, the ends of the CDNA were made blunt with Klenow fragment and EcoRI/NotI adapters (Pharmacia) were ligated to each end. The cDNA was purified from unligated adapters by spun-column chromatography using sephacryl s-300 and size-fractionated on a 1% low melting point mini-gel. Size selected cDNAs (2 - 3 kb) were removed from the gel using agarase (New England Biolabs), phenol:choloroform extracted and precipitated using 0.3 M NaOAc (pH 7)/ethanol. A portion of each cDNA size-fraction (0.1 ug) was co-precipitated with 1 ug of lambdaZapii (StratageneEcoRI digested, dephosphorylated arms and then ligated in a volume of 4 ul overnight. Each ligation mix was packaged in vitro using Giqapack II gold packaging extract (Stratagene). We have determined that although first strand cDNAs begin 8-10 bp from the poly-A tail. The reason for the loss of the poly-A tail is most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-*Yector: pBluescript SK-; Site_1: EcoR1; Site_2: EcoR1; Using 5 ug of polyadenylated mRNA from 3 day-old Arabidopsis thaliana (Columbia) seedling hypocotyls as template and oligo d(t) as primer, first strand synthesis was catalyzed by Moloney murine leukemia virus reverse transcriptase (Pharmacia). Second-strand cDNA was made using the procedure of Gubler and Hoffman (1983) except that DNA ligase was omitted. After the second strand reaction, the solds of the column was made below the second strand reaction.
                                                                                                                                                                                                                likely due to lower than anticipated nucleotide levels during the Klenow repair of ragged ends before the addition of linkers (3'-5' exo instead of 5'-3' pol). When this library is used please reference the ABRC and: Kleber, J. et al. (1993) Cell 72:427-441."
                                                                                                                                                                                            Kieber, J.
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/dev_stage="3 day-old"
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/strain="Columbia"
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                           23.4%; 97.6%;
                           Score 422.4;
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Qy

182

gtgtgaagaggaaagtttgttatttctatgaccctgaggtcggcaattactactatggcc

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                                                                      CCCGAGGTTGATGAAGACCAAGAAGATGGGGATAAAAGATGGGATCCGGATTCAGACATG 398
                9atgttgatgacgtaaacctataccaagcagagtaaaaagagaagctgttgaacca 1455
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GATGTTGATGATGACCGTAAACCTATACCAAGCAGAGTAAAAAGAGAAGCTGTTGAACCA
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                                                                                                                                                    432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: David Smoller, Ph.D.

Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P., Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and Hanson,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AI994124.1 GI:5841029
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                       service@genomesystems.com
Location/Qualifiers
                                                                                                                                                                                                                                                                /clone_lib="A, thaliana, Ohio State clone set."
/note="CDNA library was made from selected clones
Arabidopsis thaliana Ohio State clone set."
a 132 c 61 g 140 t 23 others
                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="701499210"
                                                                                                                                                                      23.2%;
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Pred. No. 1.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Genoscope
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l (bases 1 to 999)
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                                                                          /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the NotI and Eco RV sites of the pcMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                        fliang@lifetech.com URL :
                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODA011YG11"
                                                                                                                                                                                                                                                                   /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
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Query Match Best Local Similarity

22.8%;

Score 412.6; DB 9 Pred. No. 8.9e-94; Mismatches

DB 9;

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BG368908
BG368908.1 GI:13258009
EST.
                                                   BG368908 775 bp mRNA linear EST 22-OCT-200:
HVSME10021D24f Hordeum vulgare 20 DAP spike EST library HVcDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSME10021D24f, mRNA sequence.
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togetoactacggtotccttcagcatatgcaggttctcaagcccttccctgcccgcgaac

CCGGCGGGACGGCTCGAAGCGCCGCGTCTGCTACTTCTACGACGCGGAGGTGGGCAACT 184

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Development of a genetically and physically anchored EST resource for barley genomics: Morex 20 DAP spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rwing@clemson.edu
Total hq bases = 631
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  Conservative
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                                                                                                                                                                      http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Alss see Close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gppages/bgn/31/cover.html)* 280 c 216 g 121 t
                                                                                                                                                                                                                                                                                                                                                                    California, Riverside (Choi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spikes with awns trimmed were collected at 20 DAP (Fentol) Total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids in the TJ Close lab at the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whol-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="20 DAP spike"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Morex"
/db_xref="taxon:4513"
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Score 408.6; DB 10; Pred. No. 8.3e-93; 0; Mismatches 135;
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BE053804.2
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GA__Ea00
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                          Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 818.
                                                                                                                                                                                                                                                  Unpublished (2000)
On Jun 8, 2000 this sequence version replaced
Contact: Wing RA
                                                                                                                                                                                                                                                                                              Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simme, D., Mood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, of the cotton fiber
                                                                                                                                                                                                     Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                    Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gossypium
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                                                                                                                                                                          864 656 7288
864 656 4293
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA__Ba0035C07f"
/clone_lib="Gossypium arboreum 7.
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KEYWORDS SOURCE

EST

ORGANISM

Homo sapiens Eukaryota; M

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamumalia; Eutheria; Primates; Catarrhini; Hominidae;

Hominidae;

Euteleostomi;

VERSION

ACCESSION DEFINITION LOCUS

prime, mRNA: AL531607 AL531607.1

GI:12795100 sequence

AL531607 AL531607 LTI\_NFL001\_NBC4

Homo dq sapiens mRNA

CDNA

linear

CS0DM002YH15

EST 13-FEB-2001

RESULT 12 AL531607

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             gaggaaggaacaaacaagg 1612
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                                                                    agcactaaggttacaggagtaaacccagtgggagtggaggaagcaagtgtgaaaatggaa
                                                                                                                             ctgaaaggaattatggagcgtggaaaagg---ttgtgaggtggaggtggatgagagtgga 1533
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CAAGAAACATCGAACAAAG
                                                                                                           CCGAAAGGCACTGCAGAGCAAGCTAGAGGGATTCGACACATGGCAACAATGAGACCCTA
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                                                    AGTACAAAGTCTGTAGATGTCAGGCCTATGGCTATCGATGAACCAACTGTGAAAGTCGAG
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dpa"
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                                                                                           gcgtgttctttatgtcgatattgatatccaccacggggatggagtggaggaggcatttta 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gaggaaagtttgttatttctatgaccctgaggtcggcaattactactatggccaaggtca 248
                                                                                                                                                         TGGCTTCTGTTACGTCAATGATATCGTCTTGGCCATCCTGGAACTGCTAAAGTATCACCA 519
                                                                                                                                                                                                                                                                                         ctgcgatattgccatcaactgggctggtgtctccatcacgctaagaagtgcgaggcctc
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585; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope
Genoscope - Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockwille, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-*Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"LTI_NFL001_NBC4"
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braries and normalization
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Pred. No. 2.8e-90;
"Mismatches 293;
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                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp
South Memorial Parkway Huntsville, AL 35801 For further
call: (800)-533-4363 or contact via email: ccu@resgen.cc
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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                   /note-"Vector: pBluescript II XR; Site_1: EcoR1; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was XR library construction kit. Complementary DNA was
                                                                                                                                                                                                                                                                 /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                  /clone="GENOME SYSTEMS CLONE ID: Gm-c1016-6128"
/clone_lib="Gm-c1016"
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                                                                                                                                                                                                                                                                                                                                                 ACATTCACCATGGAGACGGTGTGGAGGAAGCTTTCTACACTACTGACAGAGTCATGACTG
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                                                                                                                                   AW308961 597 bp mRNA linear EST 03 sf92d04.yl Gm-c1019 Glycine max cDNA clone GENOME SYSTEMS Gm-c1019-3584 5' similar to SW:HDAC_ARATH 022446 HISTONE
                     soybean.
Glycine max
                                                               EST
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                 AW308961
AW308961.1 GI:6724562
                                                                                                               DEACETYLASE ;, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was
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Pred. No. 4.5e-89;
0; Mismatches 164
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                                                                                                                                                                 GCTCTAAAGTTGAACCATGGAGTATGTGATATTGCAATAAATTGGGCTGGTCTACAT
                                                                                                                                                                                                                                                                                                                         cccgtctttgacggcctttattccttttgccagacctatgctggaggatctgttggtggc 525
ctagagctccttaagcagcatgagcgtgttctttatgtcgatattgatatccaccacggg
                                                        CATGCAAAGAAGTGTGAGGCTTCTGGGTTTTGCTATGTTAATGACATTGTGCTGGCTATT
                                                                                    cacgetaagaagtgegaggeetetggettetgttaegteaatgatategtettagetate
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                                                                                                                                                                                                                                                                            CCTGTATTTGATGGTCTTTACTCTTTCTGCCAGACATATGCAGGAGGTTCTGTTGGTGGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Shoemaker R/Public
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="vector: psport] (Life Technologies); Site_1: Not I; Site_2: Sal I; This cDNA library was constructed from mRNA isolated from immature seed coats (200-300 mgs) of greenhouse grown plants. The library was prepared using the Life Technologies psuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the psport] vector. The Ligated cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the psport] vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHJOB host cells (Gibco BRL). This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna.*
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/clone_lib="Gm-c1019"
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BP 191 91006 EVRY cedex – France
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Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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1 (bases 1 to 847)
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AL558916
AL558916.1 GI:12903904
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                                                                 Conservative
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seqref@genoscope.cns.fr,
                                                                                                                                                                                          cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Fong Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                               http://fulllength.invitrogen.com*
195 c 224 g 207 t
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/note-"vector: pcMvSPORT 6; Site_1: Not1; lst strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I an
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/db_xref="taxon:9606"
/clone="CS0DJ007YP20"
/clone_lib="LTI_NFL008_TC2"
                                                                                                                                                                                                                                                                                                                                                        /sex="male"
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                                                                               21.48; 67.18;
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                                                              Score 386.4; DB 9
Pred. No. 3.8e-87;
1; Mismatches 267
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Search completed: April 28, 2002, 18:51:38 Job time: 7628 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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RESULT US-09-; Sequ ; Pate

S-09-282-305-5 Sequence 5, Application Patent No. 6287843

US/09282305

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APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (140)..(1459)
US-09-282-305-5
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Best Local Similarity
Matches 912; Conserv
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ORGANISM: Zea
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                415
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73.0%;
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Pred. No. 1.2e-216;
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; TYPE: DNA;
; ORGANISM: Zea mays;
; FEATURE:
; NAME/KEY: CDS;
; LOCATION: (29)..(1405)
US-09-282-305-1
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT APPLICATION NUMBER: 60/080,563
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                          SOFTWARE: Pate
SEQ ID NO 1
LENGTH: 1826
                                                                                                   Query Match 31.0%; Score 559.4; DB 4; Best Local Similarity 66.8%; Pred. No. 2.1e-171; Matches 797; Conservative 0; Mismatches 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09282305 Patent No. 6287843
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                                                                                                                                   Length 1826;
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129	1240 cttgaagagattcgcaatgaccttctccaccaatctctctaagcttcagcatgctccaagt	Ϋ́
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108	1120 geactiggagitigaagitigaagatageagatgecggageatgaatattatgaatactitiggt	B 2
111 102	1060 ggtggtggttgatacactatccgcaatgttgcccgttgctggtgctaccgacgactggagtt	, B 3
961		물
901	940 ttgcaatgtggtgctgactccctatctggggatcggttaggttagttccatctttcaatc 999	45 AG
939 841	880 ctgttattcaagcccatcatggggaaagttatggaaattttccgaccaggggctgtggta 	ОУ
879 781	820 ggaaagtactattctctcaatgtaccactggatgatggaatcgatgatgagagctatcat 	ДУ
819 721	760 cataaatttggtgattactttcccggtacaggtcacattcaggatataggttatggtagc	P 04
759 661	700 cacq999atggagtggaggaggcattttatgctactgacagggttatgactgtctcgttt	DP
699	640 gctatcctagagctccttaagcagcatgagcgtgttctttatgtcgatattgatatccace	DB Qy
639 541	580 otocatcacgotaagaagtgogaggoctotggottotgttacgtcaatgatatcgtotta	Dβ
579 481	520 ggtggctctgtcaagcttaaccacggcctctgcgatattgccatcaactgggctggtggt	Db Qy
519 421	460 gactgtcccgtctttgacggcctttattccttttgccagacctatgctggaggatctgtt	9 0 0
459 361	400 attacecetgaaacccagcaagatcagattcgccaacttaagcgcttcaatgttggtgaa	, B 5
399 301	340 gocogogaacgtgatototgocogottocacgocgacgactatgtctottttctccgcagc	P 44
241	182 cactogotggtggtccactacggcotecacggcotctccaggctctcccgcccctacccg	Db
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                                                                                                                                                                    Best
                                                                                                                                                       Matches
                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (616) 381-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                          ORGANISM: HOMO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2111
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309 tcagcatatgcaggttctcaagcccttccctgccgcgaacgtgatctctgccgcttcca
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OPERATING SYSTEM:
SOFTWARE: WORDPEN
                                                                                                87
                                                                                                                                                      Local Similarity 64.(
nes 752; Conservative
                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 64..1512
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CITY: Kalamazoo
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                             LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Terryence F. Chapman
                                                                                                                                                                                                                                        IDENTIFICATION METHOD:
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                                                                                                             gaggaaagtttgttatttctatgaccctgaggtcggcaattactactatggccaaggtca 248
                                                      tcccatgaagccccatcgcatcaccatgacccatgccctcctcgctcactacggtctcct 308
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                                        CCCAATGAAGCCTCACCGAATCCGCATGACTCATAATTTGCTGCTCAACTATGGTCTCTA
                                                                                                GAGGAAAGTCTGTTACTACTACGACGGGGATGTTGGAAAATTACTATTATGGACAAGGCCA 146
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RPDL PROTEIN AND DNA
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Pred. No. 1.8e-151;
0; Mismatches 423;
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CATCCCTGAGGAGAGTGGCGATGAGGACGAAGACG
                       agagactcccgaggttgatgaagaccaagaagatg 1363
                                                                                                               caatctctctaagcttcagcatgctccaagtgtaccatttcaggaaagaccacctgatac 1328
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; IDENTIFICATION METHOD:
US-08-717-365-2
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                                                                                                                                                                                                                                                                 Matches 752;
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                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
NEORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44

MEDIUM TYPE: Diskette, 3.5 inches, 1.44

COMPUTER: IBM PC/XT/AT Compatible

COMPUTER: IBM PC/XT/AT Compatible

COMPUTER: IBM PC/XT/AT COMPATING SYSTEM: MS-DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: Furuya Case TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: RPDL PROTEIN AND DNA TITLE OF INVENTION: ENCODING THE SAME NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
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APPLICANT:
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369 cgccgacgactatgtctcttttctccgcagcattacccctgaaacccagcaagatcagat 428
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                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP6-227876 FILING DATE: 22-SEPTEMBER-1994
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                                   CCGAAAAATGGAAATCTATCGCCCTCACAAAGCCAATGCTGAGGAGATGACCAAGTACCA
                                                                                                              CCCAATGAAGCCTCACCGAATCCGCATGACTCATAATTTGCTGCTCAACTATGGTCTCTA 206
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Pred. No. 1.8e-151;
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RESULT 6 US-09-282-305-9 ; Sequence 9, Application US/09282305 ; Patent No. 6287843 ; GENERAL INFORMATION:

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LENGTH: 1576
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Malze Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER: OF SEQ. ID NOS: 18
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NAME/KEY: CDS
LOCATION: (38)..(1336)
-09-282-305-9
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Pred. No. 9.9e-142;
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APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TIPLE OF INVENTION: Maize Histone Deacetylases And
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT APPLICATION NUMBER: 05/080,563
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                                                        ; LOCATION: (29)..(1084) US-09-282-305-3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09282305 Patent No. 6287843
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1475
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                                                                                                                                                                                                                         Local Similarity nes 530; Conserv
                                                       gtggtattgcaatgtggtgctgactccctatctggggatcggttaggttgcttcaatctt 993
cacggggatggagtggaggcattttatgctactgacagggttatgactgtctcgttt
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Pred. No. 1.7e-114;
0; Mismatches 243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                            APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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ZIP: 27709
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                                                                                                                                                                                                                f: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                USA
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Steiner, Sabine
Mohr, Christine
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                                                                                                                                                                                                                                                                                 No. 6239264artis Corporation
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Best Local Similarity 62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: (
541 TGGACGTACGAGACAGG
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                                                               GGGATACCTATGCTATGTCGGTGGTGGAGGTTACACCCCCAGGAATGTGTCGCGGCTA
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                                                                                 aatgttcccctactgctcttgggtggttggttacactatccgcaatgttgcccgttgc 1098
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RESULT 9 US-08-232-463-14/c ; Sequence 14, Application US/08232463 ; Patent No. 5670367

GENERAL INFORMATION:

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REFERENCE/DOCKET NUMBER: 3047.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)693-4109
TELEX: 899149
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APPLICANT:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                           1310 aggmaagaccacctgatacagagactcccgaggttgatgaagaccaagaagatggggata 1369
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                     1370 aaagatgggatccggattcagacatggatgttgatgatgaccgtaaacctataccaagca 1429
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1610 agggtgggggggggggggtttcctcctaaaacataagactcggagcttctaatttctt 1669
                                                                   1430 gagtaaaaagagaagctgttgaaccagatacaaaggacaaggatggactgaaaggaatta 1489
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US-08-232-463-14
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                                                                                                             1116
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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MEDIUM TYPE: Floppy disk
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                                     IMMEDIATE SOURCE:
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TELECOMMUNICATION INFORMATION:
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391 ctccgcagcattacccctgaaacccagcaagatcagattcgccaacttaagcgcttcaat 450
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: 11
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TELEX: 899149
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1800 Diagonal Road, Suite 500
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(703)683-4109
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         RESULT 12
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SEQ ID NO 17
LENGTH: 289
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Best Local
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CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
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LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C
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20; Conserv
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GENERAL SZOSTAK JACK W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
APPLICANT: Liu, Rihe
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                              Sequence 17, Application US/09007005B Patent No. 6258558
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Best Local Similarity
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TITLE OF INVENTION: SELECTION OF PROTEINS USING FILE REFERENCE: 00786/459003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                             APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W
                                                                                                                                                           APPLICANT: Liu, Rihe
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NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n =
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TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
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Pred. No. 0.00014;
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US-09-244-796-17/c; Sequence 17, Application US/09244796
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: LOCATION: (1)...(289)
: OTHER INFORMATION: n - A,T,C
US-09-007-005-17
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EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
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SEQ ID NO 17
LENGTH: 289
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Matches 19; Conserv
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NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER IMFORMATION: n = A,T,C
-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SELECTION OF PROTEINS USING TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: 05/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER FILING DATE: 1999-02-05
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Llu, Rihe
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EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                          LENGTH: 28
TYPE: RNA
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                                                                                                                      OTHER INFORMATION: Translation template
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8.6%;
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                                                                                                                                                      Query Match
Best Local Similarity
Matches 64; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sakin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: LUD 5525
FILE REFERENCE: LUD 5525
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                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                      LENGTH: 485
                                                                                              194 atgtaactgatgagcatggggaaagagggtcttttgctgaaacaga 239
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                    atgaagaccaagaagatggggataaaagatgggatccggattcaga 1391
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                                                                                                                                                                         Score 38.8; DB 4; Length 485; Pred. No. 0.016;
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Search completed: April 28, 2002, 19:24:41 Job time: 8221 sec

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Result
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Maximum DB seq length: 2000000000
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                                                                                                                830.2
740.4
734.2
698.6
559.4
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1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
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31.0
29.1
29.1
29.1
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Maximum Match 100%
Listing first 45 summaries
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9: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA199.DAT: *
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12: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA199.DAT: *
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Partial cDNA	AAT8637	227		5	41	
Human	AAF17	241		٠.	40	
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_	AAF0754	570		-	38	
cDNA encoding nove	AAS41	1016		.4	37	
Human polynucleot	AAI6131	1539		143	36	
Partial		375			35	
Partial	AAT863	379		166.6	34	
Human breast	AAH5563	402		170.4	w w	
	AAZS	541	10.3	186	32	
Human polynucleot	AAIS	2046	11.7	211	31	
Human histone deac	AAZ9332	1654		211	30	
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Drosophila		1662		381.8	24	
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	2 AAC89556	1954	•		20	
Maize histone		1576		468	19	
Drosophila melanog	3 ABL01897	2145	•		18	
RPDL transcription		2111		•	17	
Human prostate	1 AAF16188	2163	•	•	16	
Human histone	2 AAC89554	1611			15	
cDNA encoding		1449	•	•	14	
Human histone	2 AAC89555	1985			13	
U31814 cDNA clone	AAC	1985		504.4	12	
Human METH2	AAZ3206	1985		•	11	

## ALIGNMENTS

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                                                       24-AUG-2000; 2000CA-2316036
                                                                       27-FEB-2001.
                                                                                        CA2316036-A1.
                                                                                                                                                                  Histone deacetylase; AtRPD3A; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation; ds.
                                                                                                                                                                                           Nucleotide sequence of a histone deacetylase designated AtRPD3A.
                                                                                                                                                                                                             29-JUN-2001
      Brown D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
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RESULT
AAZ58260
                                    Query Match
Best Local Similarity
Matches 1021; Conserv
                                                                                                                                                                                              The present sequence is that of cDNA clone sr1.pk0023.dl encoding soybean histone deacetylase | (HDI, see AAYSB829), a chromatin associated protein. The cDNA clone was isolated from a soybean root cDNA library on the basis of homology to other plant histone deacetylases. The invention relates to isolated rice, soybean and wheat nucleic acid fragments encoding HDI. It also relates to the construction of a chimeric gene encoding all or a portion of HDI, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HDI in a transformed host cell. The availability of nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in enkaryotic cells,
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                                                      altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter; RNA polymerase II; transcription; plant transformation; heterochromatin; disease registance; chromatin assembly; gene activity; toxin screening;
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                                                                                                                                                                            The present sequence encodes a maize histone deacetylase. This DNA belongs to family 1, ZmHDl and appears to be regulator of promoters RNA polymerase II, for transcription of genes. The nucleotide sequences be used to transform plants and increase disease resistance by
                                                                                                                                                                                                                                                                                                                                 Claim 1;
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CC (see AAV58828) of rice histone deacetylase 1 (HD1), a chromatin CC associated protein. The contig was obtained from cDNA clones isolated from rice callus, 15-day-old leaf and 15-day-old seedling CC isolated from rice callus, 15-day-old leaf and 15-day-old seedling CC cDNA libraries on the basis of homology to other plant histone CC deacetylases. The invention relates to isolated rice, soybean and CC wheat nucleic acid fragments encoding HD1. It also relates to the CC construction of a chimeric gene encoding all or a portion of HD1, CC in sense or antisense orientation, where expression of the chimeric CC gene results in production of altered levels of HD1 in a CC transformed host cell. The availability of nucleic acid sequences cenceding (portions) of histone deacetylase proteins will facilitate CC studies of global transcriptional regulation in eukaryotic cells,
                                                                                                                                                                                                                              Claim 3; Page 24; 36pp; English.
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                                 RNA polymerase II, for transcription of genes. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promote RNA polymerase II; transcription; plant transformation; heterochromatin disease resistance; chromatin assembly; gene activity; toxin screening;
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                                                                                                                                                                   New deacetylase genes, used increased disease resistance
                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC
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                     response promoters
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                                                       tggtggtggttacactatccgcaatgttgcccgttgctggtgctacgagactggagttgc
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                                                                          altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter RNA polymerase II; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1242
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                                                                                                                                                             The present sequence encodes a maize histone deacetylase. This DNA belongs to family 1, ZmHDl and appears to be regulator of promoters for RNA polymerase II, for transcription of genes. The nucleotide sequence can be used to transform plants and increase disease resistance by
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  Sequence 1826 BP; 437 A;
                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                            New deacetylase genes, used for producing transgenic increased disease resistance -
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                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes an Arabidopsis thaliana histone deacetylase designated AtRPD3B. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative
                                                                                                                                                                                                                                                                                                        association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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                                                                                                                                                                               respectively. METH1 and METH2 have been found to be potent inhibitors of cancer and other disorders related to angiogenesis both in vitro and in vivo. They can be used for treating ceancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psorlasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis, AAZ32080, and AAY49503 to
                                                                                                                         Query Match
Best Local
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(HAST/)
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                                                                                                                                                                               Sequence
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20-JUL-1999;
10-AUG-1999;
13-AUG-1999;
22-DEC-1999;
22-FEB-2000;
          The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003). The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
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) FORNWALD J A.
) TERRETT J A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms neoplasia, or for inhibiting neoplastic cell growth in an animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1338 cgaggttgatgaagaccaagaagatg 1363
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                                                                                                                                                   Sequence
                                                                                                                                                                                                         The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-6 and HDAC-D. These inhibitors may be antisense strands or they may be compounds identified by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and for identifying which histone deacetylase is involved in a neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                        The present cDNA sequence encodes a novel histone deacetylase (HDx) polypeptide, designated HD1. The HDx polypeptides are capable of modulating proliferation survival and differentiation of cells. The proteins are able to alter chromatin structure by deacetylating histones such as H3 or H4. They have the ability to modulate cell growth by influencing cell cycle progression or to modulate gene transcription. The products can be used for diagnossis and therapy. They can be used, for example, to treat tumours or proliferative disorders or spermatogenesis, osteogenesis, chondrogenesis or the differentiation of progenitor cells. They can also be used to treat psoriasis, bone diseases,
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                        fibroproliferative disorders, degenerative disorders, or for repair of cartilage, increasing bone density, liver repair subsequent to a partial hepatectomy, to promote regeneration of lung tissue in the treatment of emphysema, or for inducing tolerance in autoimmune diseases, and transplant recipients. Hox inhibitors can be used as anti-fungal agents, preservatives in foodstuff, feed supplements for promoting weight gain illuestock, disinfectants, insecticides or defoliants. The products can be considered to the products of the products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated histone deacetylase polypeptide(s) and genes -develop products for modulating the proliferation, survival differentiation of cells, e.g. for treating tumours.
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                             tgcccggtgctggacatatgagacagctgtggccctggatacggagatccctaatgagct
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64.1%;
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Pred. No. 1.4e-142;
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Best Local 9
                                                                                                                                                                                                                                                                                                                      The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These inhibitors may be antisense strands or they may be proposed the compound and measuring the resulting by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and identifying which histone deacetylase is involved in a neoplasia.
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## ALIGNMENTS

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/organism-"Arabidopsis thaliana" /db_xref-"taxon:3702" 472 a 386 c 464 g 485 t	1. 1807	Location/Qualifiers	The Minister of Agriculture and Agri-Food (CA)	Patent: EP 1094112-A 1 25-APR-2001;	Repressing gene expression in plants	Wu,K., Miki,B.L., Tian,L. and Brown,D.C.	1 (bases 1 to 1807)	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	<pre>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;</pre>	Arabidopsis thaliana	thale cress.		AX139014.1 GI:14274698	AX139014	Sequence 1 from Patent EP1094112.	AX139014 1807 bp DNA linear PAT 30-MAY-2001		

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Direct Submission

Submitted (18-OCT-1999) Eastern Cere
Agriculture and Agri-Food Canada, Ot
Location/Qualifiers

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/codon_start=1
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VNDIVLAILELLKQHERVLYVDIDIHHGDGVEBAFYATDYMTVSFHKFGDYFPGTGH
IQDIGYSGKYYSLNVPLDDGIDDESYHLLFKPIMGKVWEIFRPGAVULQCGADSLSG
DRIGCTNLSIKGHAECYKFMRSFNVPLLLLGGGGYTIRNVARCWCYETGVALGVEVED
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PPDTETPEVDEDQBGDKRWDDDSDMDYDDBRKPIPSRVKREAVEPDTKDKDGLKGIM
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Submitted (16-JUL-1997) Department of Biology, Central Research
Institute of Electric Power Industry, 1646, Abiko, Chiba 270-11,
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Characterization of a histone deacetylase (
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MTHALLAHYGLLQHMQYLKPFBAREDLGERFHADDYSFLRSIT PETQQDQIRQLKRY
NVGBDCPVFBGLYSFQGYYAGGSVGGSVKLNHGLCDLAINMAGGLHHAKCEBAGFCY
VNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGH
IQDIGYGSGKYSLNVFLDDG LDDESYHLLFR IMGKYMEIFREAVVLQCGADSLSG
DRLGCPNLSIKGHAECYKFMRSENVPDLLLLGGGYTIHVARCWCYETGVALGVEVEB
KMPEHEYYEYFGPDYTLHVAPSNMENKNSROMLEEIRNDLLHNLSKLQHAPSVPFQER
PDTTETPFVDEDGEDGNKWDDEDSDMDVDDDRKPIPSEAVKREAVEDTTMCKCOCKGIM
ERGKGCEVEVDESGSTNVTGVNPQVEEASVKMEEEGTNKGGAEQAFPPKT"

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/protein_id-"AAB66486.1"
/db_xref-"G1:2318131"
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                                     Submitted (26-FEB-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
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Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosome 4 can
viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative protein"
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/fb_xref="GI:4467095"
/fb_xref="GI:4467095"
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fprsetrpdsvycsptipcoswsataistpspsllaspklocdtsgdvyptrnrspls
fflsvssssstpsspkspasfsllkskloctycvtlnrnnossissskkgftclasakag
rgtaiftaecshtehfpcvasragdrullsdcvyrgfntipesnrdeeeebnddgefkkf
gsdskirgsknnnkslrvynddbeplisspisrgfntipesnrdeeeebnddgefkkf
fvutpsplittkmltdsvtghvyndbeplissplsrggnetysvlmkikspslptarr
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spvdlyvddisgdomsvndavkkakvtedbroknlftifutbrnrnsahoag
lagpdfvtstrfshleipthtiwlgachhalpddyfarriksllslsvddlyndryndssglsgrpwilsgelfardomsparrikspslsgrssksrggrimtr
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/PROCESSIANO
/PROC
                                                                                                                                                                                                                                                                                                               Contains Eukaryotic putative RNA-binding signature [KGSCFLPM] contains EST gb:N97112;AA728688*
                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(9755. .10264, 12071. .12191,12300. .12463))
//gene="F20D10.20"
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12071...12191,12300...12463))
/gene="f20D10.20"
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/gene="F20D10.10"
/note="strong similarity to retrotransposon -like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(830.../gene="F20D10.10"
830...3049
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YSGAERMLTSARALLVQYGLSSSDSCLRGLEAELADLNRLRGRHVAVKSPEPVVQKSE
PLTPTSAWRAAERLAKVAIMRHMNRVSDLHGFENARF*
                                                                                                                                                                                                                                   /product="putative protein"
/protein_id="CAB37530.1"
                                                                                                                                                                                                                                                                                                                                                                                                      gene F32B5.7, PID:g2088783
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/gene="F20D10.10"
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/number=1
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/variety="Columbia"
/db_xref="taxon:3702"
/chromosome="4"
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                                                                                                                                                                                                                                                                                             /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similarity to Caenorhabditis
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/gene="F20D10.20"
/number=4
complement(14739.
/gene-"F20D10.30"
/number-2
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TURGEVER AND TENARGES TYPE VICAPPEC SEPVEND VIGIDLG
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PPTRSFTVLHLVQARPSLKGSCFLPMLKKVRLAKSFTRVVDETETEVINLOMRNSNDA
APKGDRRQVIGVKEGETTVLAEVDFTFWSLLDSKWSLKOTCNPATDGPLFELSGTRM
VKVYSGRKLEKEPKHGSKLRSEODFMTAVEFSKQHPYGKAVGLLDLKFGSIEANEKWLL
VLPGMVSSFILSDLLKKEGFSAAAKDTVKANGITEESTEIDVLSQEKLEEETMMDVDT
TTPVAVAAEKINGGAROFSKELSGNMIEEEEGGHCGGCGGCGGGGGCGGGGRCGGM
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complement()01n(13386. .14030,14118. .14738,1482
15491. .15569,15669. .15730,16043. .16069))
/gene="F20D10.30"
/note="strong similarity to dnaK-type molecular
PHSP1 -Pisum sativum, PID:g20835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(13386. .14030,14118. .14738,14828. .15394,
15491. .15569,15689. .15730,16043. .16069))
/gene=*F20D10.30*
13386. .16069
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/gene="F20D10.20"
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/gene="F20D10.20"
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                                                                                                           /gene="F20D10.30"
                                                                                                                                                                                                                       complement(14031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="heat shock protein
/protein_id="CAB37531.1"
/db_xref="G1:4467097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contains ATP/GTP-binding site motif A (P-loop) [AEAYLGKS],
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/number=5
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                                                                                       TATTGCCATCAACTGGGCTGGTGGTCTCCATCACGCTAAGAAGTGCGAGGCCTCTGGCTT
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                                                                                                                                                                                                                                                                                CCAGACCTATGCTGGAGGATCTGTTGGTGGCTCTGTCAAGCTTAACCACGGCCTCTGCGA
                                                                                                                                                                                                                                                                                                         ccaqacctatgctggaggatctgttggtggctctgtcaagcttaaccacggcctctgcga
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                                                           CTGTTACGTCAATGATATCGTCTTAGCTATCCTAGAGCTCCTTAAGCAGCATGAGGTTTG 86543
                                                                                                                                                                                                                                                                                                                                                                                         ACTTAAGCGCTTCAATGTTGGTGAAGACTGTCCCGTCTTTGACGGCCTTTATTCCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATGCAGGTTCTCAAGCCCTTCCCTGCCCGCGACCGTGATCTCTGCCGCTTCCACGCCGA 86843
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Pred. No. 1.1e-258;
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Gaps

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LCRSFVLAPTPPTQNVNNAHSSSTLYLSIFFFFCIFLHLLGYL"
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/gene="AT4938140"
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                           /product="putative protein"
/protein_id="CAB80481.1"
/db_xref="GI:7270800"
                                                                                                                                              /note-"contains EST gb:AI992903.1, H37273, AI100213, T41873, AA067478, AI100538"
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10151. .11059
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/protein_id="CAB80479.1"
/db_xref="GI:7270798"
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Arabidopsis thaliana, PID:g3790554"
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/note="eimi"
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/numher=1
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translation="mevTNTSSIMWFFRDKGFDDPSIDKMLRKCKQLEKAQSDVASEN/
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ccagacctatgctggaggatctgttggtggctctgtcaagcttaaccacggcctctgcga
                                                      AGAGGTAATGGATACTGGCGGCAATTCGCTGGCGTCCGGACCTGATGGTGTGAAGAGGAA
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PPILSHSVEEKLCPLLAFFQALGVPETQJGKMILFNPRILTSYSLDTKLTVIVSFLASI.
GLDQDGMIGKYLVKNPETLMGYSYDKKLRPTTEFLKSSVGLSEDGJKSVVMNFPQLLCS.
DVNKILKPNYDYLKECGFGDSQIATMVTGYPQILIKSVKNSLQPRIFFLVQVMGRGMD
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GTRLPNGEAYPSEEARETANATNIPGGEKERT1LELTAELERTGQRCEVYRANLLS1L
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SPMEKQAASLYTRAAFIKFQEEFVETLAIPANIISDSGTHTTYRVAKFGEVHKGHTVS
FDSLEVKANCSCQMFEYSGIICRHILAVFSAKNVLALPSRYLLRRWTKEAKIRGTEEQ
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yfgdptlyfdtyrgkryovpfaaftgfnhhgopvleggallesessfamlfotwel
Qamsapppsgttyeddrliovavsryvesotrlikfsopvlegfeklahypgahfte
sefincytetetaaefeasmdsivrryymedndmlosiynaroomvrvfirdtfygel
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attachment site AA73-83
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13703. .15130
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/protein_id="CAB80482.1"
/db_xref="GI:7270801"
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/gene="AT4g38170"
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Pred. No. 1.2e-258;
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Query Match  Best Local Similarity 72.1%; Pred. No. 7.8e-213;  Matches 1035; Conservative 0; Mismatches 400; Indels 0; Gaps 0;  91 ttgactgcgactgtgattacaacaccgttgatcctacgaaaagaggtaatggatact 150	4468 a	ď	AF282858  AF282858  ION Mesembryanthemum crystallinum histone des complete cds. AF282858  AF282858.1 GI:9022438  S common ice plant. ISM Mesembryanthemum crystallinum Eukaryota; Viridiplantae; Streptophyta; losses to 1839)  Spermatophyta; Magnoliophyta; eudicotylec Caryophyllidae; Caryophyllales; Aizoaceae CE 1 (bases to 1839)  RS Scharte, J. and Baur, B.

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1503 GACGATGTCAAGGATGCTGTGGATCATCCAAGAGACATGGATGTCGTATGGTG

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1471 gatggactgaaaggaattatggagcgtggaaaaggttgtgaggtggaggtggatg
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Baldwin, D.Adelphi., Briggs, S.P. and Crans
Malze histone deacetylases and their use
Patent: US 6287843-A 7 11-SEP-2001;
Location/Qualifiers
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                                                                                                                                                               Song, F. and Goodman, R.M.
Song, F. and Goodman, R.M.
Direct Submission
Submitted (30-DEC-2000) Department of Plant Pathology, University
Submitted (30-DEC-2000) Tago Linden Drive, Madison, WI 5706, USA
                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1579)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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TCAGTGCGGCGCTGATTCGTTGTCCGGCGATAGGTTGGGCTGTTTCAATCTCTCAGGGAA
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                                                                                                                             GAAGTATTACTGCCTGAATGTCCCGGCTGGATGATGGGATTGATGATGACAGCTACCAGTC
                                                                                                                                                                                                                                                          TGGGGATGGTGGAGGAGGCGTTTTACACGACGGACAGGGTGATGACGGTCTCGTTCCA
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EAKDQHGKRLTTEHKGPEPMADDPGSSKQAPVSRRLLYPSANP*

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Pred. No. 3.7e-190;
0; Mismatches 324;
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(Zea mays L.) that is able to complement an rpd3 null mutant c
Saccharomyces cerevisiae
Mol. Gen. Genet. 258 (3), 288-296 (1998)
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l (bases 1 to 2047)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Baldwin,D.Adelphi., Briggs,S.P. and Crane,V.C.
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1 (bases 1 to 1742)
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PHRIKHAHSLIVHYGLHRLLELSRPYPASEADIRRHSDDYYAFLASARGNGVLDPR
AIKRRWGEDCPVPEDGIPPFCQASAGGSIGAAVKLNRGDADITVNWAGGLHHAKKSEA
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DSLAGDRLGCFNLSVKGHADCLRFLRSYNVPMHVLDLENIKNNILENLKKIEHVPST
VEDDNKLFYNDYYYEYFGPDYTLHIQPKSVENLMTTKDLENIKNNILENLKKIEHVPST
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Sequence 1 from patent US 6287843.
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Baldwin, D. Adelphi., Briggs, S.P. and Crane, V.
Maize histone deacetylases and their use
Patent: US 6287843-A 1 11-SEP-2001;
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                                                  99t99t99t99ttacactatcc9caat9ttgccc9ttgctggtgctacgagactggagtt
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                                                                                         GGTGGTGGAGGTTACACCATCAGAAATGTTGCACGCTGCTGCTGCTACGAGACCGCAGTT
                                                                                                                                                              aaaggtcatgctgagtgcgtcaaatttatgagatcgttcaatgttcccctactgctcttg
                                                                                                                                                                                                    ttgcaatgtggtgctgactccctatctggggatcggttaggttgcttcaatctttcaatc
                                                                                                                                                                                                                                                                                  ctgttattcaagcccatcatggggaaagttatggaaattttccgaccaggggctgtgggta
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                                                                                                                                                                                                                                                                                                                                                                     CACAAGTATGGGGGATTTTTTCCCTGGTACTGGACATATCACTGACGTTGGGGCAGCCGAA
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                                                                                                                                              AAGGGTCATGCTGACTGCCTCCGTTTCCTTAGGTCGTACAATGTTCCTATGATGGTTTTA
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Mismatches

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No. 1.1e-145;

Local

Similarity

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AAGCCCCACCGCATCCGAATGGCCGCACTCGCTGGTGCTCCACTACGGCCTCCACCGCCTC aagccccatcgcatccgcatgacccatgccctcctcgctcactacggtctccttcagcat 315 GTCAGCTATTTCTACGAGCCGTCGATCGGAGACTACTACTACGGGCAAGGTCACCCGATG

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BASE COUNT
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Sidorenko, L., Selinger, D., Kaeppler, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chandler, V.L., Kaeppler, S.M., Kaeppler, H.F. and Cone, K.C. Sequences from the Plant Chromatin Consortium (NSF Plant project 9975930)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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asagsigaavklnegdaditvmagglhhakkseasgeryvndivlailellkeher

vlyvdidyhaddeeakefttnnvmtvsfhkyddefpctyvndivlailellkeher

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relrsynvpmyvlggggytirnvarcwcyetavavgebdnklyvndyyeyfgdpttl

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/protein_id="AAL33653.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cttaagcgcttcaatgttggtgaagactgtcccgtctttgacggcctttattccttttgc 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgeaggiteteaageeetteeetgeeeggaaegtgatetetgeegetteeaegeegae
                                                                                                           cccgaggttgatgaaga 1352
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                                                                                                                                                                                                                                                                                                                          gaaaataagaattctcgtcagatgcttgaagagattcgcaatgaccttctccacaatctc 1275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGGTTGCTTCAACCTGTGTGAAGGGTCATGCTGACTGCCTCCGTTTCCTTAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttaggttgcttcaatctttcaatcaaaggtcatgctgagtgcgtcaaatttatgagatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTATCGATGACACCACCTTTCGTGGTCTGTTTCAATGCATCATTAAGAAAGTTATGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggaatcgatgatgagagctatcatctgttattcaagcccatcatggggaaagttatggaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCGAGTCATGACTGTTTCCTTTCACAAGTATGGGGGATTTTTTCCCCTGGTACTGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTATATGTAGACATTGATGTCCACCATGGAGGATGGCGTGGAGGAGGCCTTCTTCACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctttatgtcgatattgatatccaccacggggatggagtggaggcattttatgctact 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgttacgtcaatgatatcgtcttagctatcctagagctccttaagcagcatgagcgtgtt 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCACCGTCAACTGGGCGGGCGGCCTCCACCACGCCAAGAAGAAGAGCGAGGCCTCCGGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagacctatgctggaggatctgttggtggctctgtcaagcttaaccacggcctctgcgat 555
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                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Yamada,K., Banh,J., Chan,M.,M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C.J., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JAN-2002) Plant Gene Expression Center, 800 Buchan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki.M., Narusaka,M., Ishida,J., Satou.M., Kamiya,A., Sakural,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriuni, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin Neumann, G., Kawai, J., Kim, C., Lam, B. Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinnzaki, K., Dayis, R.W., Ecker, J.R. and Theologis, A.
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Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as Pls.
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AY072201
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/product="putative histone
/protein_id="AAL60022.1"
                                                                                                                                                                                                                                                ecotype: Columbia"
1. .1704
                                                                                                                                                                                                                                                                                            /clone="RAFL09-59-F23 (R12957)"
/note="This clone is in a modified
(FLC-1) as a BamHI/XhoI insert.
                                                                                                        /gene-"At5g63110"
                                                                                                                                    76. .1491
                                                                                                                                                             /gene="At5g63110"
                                                                                                                                                                                                               /gene="At5g63110"
                                                                                                                                                                                                                                                                                                                                                                               /chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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5

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BASE COUNT
ORIGIN
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ### atgatatogtottagotatoctagagotottaagotottatgtog
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GRCYVNDIVLGILELLKMFKRVLYIDIDDVHHOGOVEEARYTTDRVMTWSFHKFGDFFP
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SLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGGGYTIRNVAKCWCYETAVAVGV
EPDNKLPYNEYFEYFGPDYTLHVDFSPMENLATPKDMERIRNTLEDLSGLIHAPSVQ
EPDNKLPYNEYFEYFGPDYTLHVDFSPMENLATPKDMERIRNTLEDLSGLIHAPSVQ
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STGEDEMDDNREPDVNPPSS"
1492. .1704
/gene="At5q63110"
a 363 c 433 g 454 t
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Pred. No. 1.2e-136;
0; Mismatches 395; Indels
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                    agcatgctccaagtgtaccatttcaggaaagaccacctg 1324
                                                                                                                                                        atgaatactttggtccagactatacacttcacgttgctccaagtaacatggaaaataaga 1225
                                                                                                                                                                                                             ATGAGACTGCAGTTGCTGTTGGAGTAGAGCCGGACAACAACTCCCTTACAATGAGTATT 1111
                                                                                                                                                                                                                                 coctactgctcttgggtggtggttacactatccgcaatgttgcccgttgctggtgct 1105
                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAGGCAGTTGTTCTTCAGTGTGGGTGCTGACTCCTTAAGTGGTGATCGGTTGGGTTGCT
TACACGCACCTAGCGTCCAGTTTCAGCACACCACCACCAG
                                                                                         attetegteagatgettgaagagattegeaatgacetteteeaeaatetetetaagette
                                                                                                                                       TTGAGTATTTCGGCCCAGATTATACGCTTCATGTCGACCCAAGTCCTATGGAGAATTTAA 1171
                                                                     ACACGCCCAAAGATATGGAGAGGATAAGGAACACGTTGCTGGAACAACTTTCGGGACTAA 1231
                                                                                                                                                                                                                                                                                                                                                       TCAACTTATCAGTCAAGGGTCACGCTGATTGCCTTCGGTTCTTAAGATCTTACAACGTTC
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1270
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Search completed: April Job time: 9248 sec 28, 2002, 19:26:38

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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2722
1 MDTGGNSLASGPDG
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDTGGNSLASGPDGVKRKVC.....KMEEEGTNKGGAEQAFPPKT 501
                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                      sp_organelle:*
sp_phage:*
                                                                                                                            sp_mhc:*
                                                                                                                                              sp_mammal: *
                                                                                                                                                               sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	В	ID	Description
_	2719	99.9	501	10	Q9SZL3	Q9szl3 arabidopsis
2	2134.5	78.4	500	10	Q9LKG1	
w	1958.5	72.0	493	10	Q9AXF0	Q9axf0 oryza sativ
4	1568.5	57.6	471	10	Q9FML2	
5	1561.5	57.4	471	10	Q9FVE5	Q9fve5 arabidopsis
6	1548	56.9	458	10	Q9ZTP8	09ztp8 zea mays (m
7	1496.5	55.0	521	ъ	077213	077213 drosophila
8	1496.5	55.0	521	ű	Q9VZA1	Q9vzal drosophila
9	1374	50.5	428	11	Q99PA0	Q99pa0 rattus norv
10	1361.5	50.0	687	w	Q9P4F5	Q9p4f5 emericella
11	1359	49.9	428	11	Q9JM08	Q9jm08 mus musculu
12	1358	49.9	428	11	Q9JLX5	Q9jlx5 mus musculu
13	1336	49.1	405	w	059702	059702 schizosacch
14	1334	49.0	465	ъ	062339	062339 caenorhabdi
15	1329.5	48.8	648	w	90106	Q9c1c6 cochliobolu
16	1320.5	48.5	444	ď	Q9GUA8	Q9gua8 cryptospori
17	1313	48.2	438	ъ	Q9VNC2	Q9vnc2 drosophila
18	1307	48.0	449	υī	Q9XYC7	Q9xyc7 plasmodium
19	1298	47.7	419	10	OGMINE	O9min6 arahidoneis

Query Match Best Local Similarity

99.98;

Score 2719; DB 10; Pred. No. 5.3e-205;

Length 501;

<b>4</b>	4.4		42																		24	23	22	21	20
293	296.5	296.5	297	298.5	299.5	301.5	309	317.5	340	367.5	389.5	425.5	448.5	475	594.5	644.5	759.5	847	847	852	1006	1138	1194	1240	1259
10.8	10.9	10.9	10.9	11.0	11.0	11.1	11.4	11.7	12.5	13.5	14.3	15.6	16.5	17.5	21.8	23.7	27.9	31.1	31.1	31.3	37.0	41.8	43.9	45.6	46.3
577	1066	1063	310	1215	142	425	1108	380	883	158	389	367	389	375	223	256	428	377	377	377	481	429	409	437	566
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Q9LS38	Q9NZS3	Q9NSW6	067877	094975	Q9M1N8	Q9SJE6	09FN07	Q9HXM1	Q9XYX1	Q9LXN8	Q99TC9	Q9WX04	Q9K7X1	067135	09н368	Q99PA2	Q9GRP1	Q9D0K6	Q9NYH4	Q9NP76	Q9P4F4	Q9GT74	Q9FH09	Q9GU59	Q9HDT2
Q91s38 arabidopsis	Q9nzs3 homo sapien	Q9nsw6 homo sapien	06 <b>7877 aquifex aeo</b>	094975 homo sapien	Q9mln8 arabidopsis	Q9sje6 arabidopsis	Q9fnq7 arabidopsis	Q9hxml pseudomonas	Q9xyx1 drosophila	Q91xn8 arabidopsis	Q99tc9 staphylococ	Q9wx04 streptomyce	09k7xl bacillus ha		Q9h368 homo sapien	Q99pa2 rattus norv	Q9grp1 leishmania	ď,			Q9p4f4 emericella	09gt74 tetrahymena	Q9fh09 arabidopsis	Q9gu59 cryptospori	Q9hdt2 ustilago ma

## ALIGNMENTS

DR DR	DR RA	R R R R R R	R R R R	RA RA	8 8 8 8 8 8	RESULT Q9SZL3 ID Q AC Q DT 0 DT 0 DT 0
InterPro; IPR000286; His_deacetylse. Pfam; PF00850; Hist_deacetyl; 1. PRINTS; PR01270; HDASUPER. SEQUENCE 501 AA; 56023 MM; 857D2E3D16B7CC1F CRC64;	SEQUENCE FROM N.A.  EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  EMBL; AL03538; CAB3753.1;  EMBL; AL161593; CAB80478.1;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Wedler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,  Mayer K.F.X.;  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  [4]	[2] SEQUENCE FROM N.A. SUDMITTED FROM SEQUENCING PROJECT; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.	NCBI_TaxID=3702; [1] SEQUENCE FROM N.A. Bevan M., Wedler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.	ASE. 4G38130, iana (Mouse-ear ciplantae; Streptcagnoliophyta; eucosicales; Brassic	ILT 1  ZL3  Q9SZL3  PRELIMINARY; PRT; 501 AA.  Q9SZL3;  Q1-MAY-2000 (TrembLrel. 13, Created)  Q1-MAY-2001 (TrembLrel. 13, Last sequence update)  Q1-JUN-2001 (TrembLrel. 17, Last annotation update)

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Query Match
Best Local Similarity
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                                                                     Matches
                                                                                                                                                                                          Scharte J., Baur B.;

Molecular cloning of histone deacetylase from crystallinum.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ EMBL; AF282858; AAF82385.1; -.

EMBL; AF282859; AAF82385.1; -.

InterPro; IPR000286; Hist_deacetylse.

Pfam; PF00850; Hist_deacetyl; 1.

PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesembryanthemum crystallinum (Common ice plant).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Alzoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation updat
HISTONE DEACETYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LKG1;
                                                                                                                                                                                                                                                                                                                                                                           TISSUE-LEAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-3544;
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YAGGSYGGSYKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIYLAILELLKQHERVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKMEEEGTNKGGAEQAFPPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNSRQMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPLLLLGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKMEEEGTNKGGAEQAFPPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNSRQMLEEIRNDLLHNLSKLOHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPLLLLGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGI
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                                                                     Conservative
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                                                                                                                                                                               56264 MW;
                                                                                       78.4%;
79.8%;
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                                                                 ; Score 2134.5; DB 1; Pred. No. 3.5e-159; 31; Mismatches 61;
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                                                                                                                                                                            CFD4FE0525209ABC CRC64;
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                                                                   61;
                                                                                                                                                                                                                                                                                        databases
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                                                                                                           Length
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SEQUENCE
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Eukaryota, Viridiplantae, Streptophyta;
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01-JUN-2001 (TrEMBLrel. 17, Last ann
HISTONE DEACETYLASE HD1.
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Song F., Goodman R.M.;
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Ehrhartoideae; Oryzeae; Oryza
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                                                                                                                                                                                              4 GGNSL-ASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVL
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                      GGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVD
                                                              KPFPARERDLCRFHADDYVSFLRSITPETQODQIRQLKRFNVGEDCPVFDGLYSFCQTYA
                                                                                                                                                      GGNSLPTAGADGAKRRVCHFYDAEVGNYYCGQGHPMKPHRIRMTHALLAHYGLLDQMQVL
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Lillopsida; Poales; Poaceae;
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DNA Res. 4:401-414(1997).

EMBL: AB008265: BAB10553.1: -.
InterPro: IPR000286; His_deacetylse.
Pfam; PF00850; His_deacetyl; 1.
PRINTS: PRO1270: HDASUPER.
SEQUENCE 471 AA; 52651 MM; CA16C2640D1B1732 CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.

MCBI_TaxID=3702;
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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YIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDG
                              YVDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDG 239
                                                                                                                                                                       TYAGGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVL 179
                                                                                                                                                                                                                                SRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCR 123
                                                                                                                                                                                                                                                                                          LKPFPARERDLCRFHADDYVSFLRSITPETQQD--QIRQLKRFNVGEDCPVFDGLYSFCQ 119
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1568.5;
Pred. No. 7.8e
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"Functional analysis of RPD3 histone deacetylase
Arabidopsis thaliana.";
Submitted (oCT-1999) to the EMBL/GenBank/DDBJ day
EMBL; AF19554B; AAG2B475.1;
Interpro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUDER.
SEQUENCE 471 AA; 52720 MW; 371BF7040E508849
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Q9FVE5; O1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLREL. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPDsb.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varnoliophyta; eudicotyledons; core_eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis
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                                                                                                                   ASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVL
                                                                                                                                  TYAGGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVL
                                                                                                                                                                                            LKPFPARERDLCREHADDYVSFLRSITPETQQD--QIRQLKRFNVGEDCPVFDGLYSFCQ 119
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                                                                                                                                                                           SRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCR
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MDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSY
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                                                                                                                                                                                                                                                                                                               57.48;
                                                                                                                                                                                                                                                                                              %; Score 1561.5;
%; Pred. No. 2.8e
64; Mismatches
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deacetylase homologs
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Matches 280
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01-MAY-1999
01-JUN-2001
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Pipal A., Wegener S.;
Pipal A., Wegener S.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF045473; AAD10139.1;
Mendel; 39025; Zeama; 3043;39925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl Panicoideae; Andropogoneae; Zea.
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Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
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                                                                                          GGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQM
                                                                                                                                                                                               LLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLL
                                                                                                                                                                                                                                                                                                     HCDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYH
                                                                                                                                                                                                                                                                                                                                                                                                                GGSYKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKNSRQMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDS---
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                                                                                                                                                                                                                                                                                                                                                                                  GAAVKLNRGDADITVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKFHRRVLYVDIDVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRV--LDEPEDDMETRPKPRXWSG 421
                                                            GGGGYTIRNVARCWCYETAVAVGVEPDNKLPYNDYYEYFGPDYTLHIQPKSVENLNTTKD
                                                                                                                                                                                                                                                                            HGDGVEEAFFTTNRVMTVSFHKYGDFFPGTGHITDVGAAEGKHYALNVPLSDGIDDTTFR
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(TrEMBLrel. 10,
(TrEMBLrel. 17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.9%;
63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50940 MW; A62775068225BE79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
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, Last sequence up
, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity
Matches 268; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             077213;
077213;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1998) to the EMBL/GenBank/DDBJ EMBL; AF086715; AAC61494.1; -. FlyBase; FBgn0015805; Rpd3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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426
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                                                                                                                                                                                                                                          YATDRVMTVSFHKFGDYFPCTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK
                                                                                                                                                                                                                                                                                                                                                                                                              KRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPSRV-KREAVEPDTKDKDGLK 447
                                                     ENLRMLPHAPGYQIQAIPEDAINDESDDEDKYDKDDRLPQSDKDKRIYPENEYSDSEDEG
                                                                     HNLSKLQHAPSVPFQERPPDTETPEVDED------
                                                                                                                                       VARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSROMLEEIRNDLL
                                                                                                                                                                   ASEICINWGGGLHHAKKSEASGFCYVNDIVLGILELLKYHQRVLYIDIDVHHGDGVEEAF
                                                                                                                                                                                                                                                                                                             LCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAF 195
                                                                                                                                                                                                                                                                                                                                         HSDEYVRFLRSIRPDNMSEYNKQMQRFNVGEDCPVFDGLYEFCQLSAGGSVAAAVKLNKQ
                                                                                                                                                                                                                                                                                                                                                                                                KKRVCYYYDSDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATADEMTKF 65
EGGRRDNRSYKGQRKRPRLDKDTNSNKASSETSSEIKDEKEKGDGADGEESTASNT
                                                                                                             VSRCWTYETSVALAVEIANELPYNDYFEYFGPDFKLHISPSNWTNQNTSEYLEKIKNRLF
                                                                                                                                                                                                VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLLGGGGGYTIRN
                                                                                                                                                                                                                            YTTDRVMTVSFHXYGEYFPGTGDLRDIGAGKGKYYAVNIPLRDGMDDDAYESIFVPIISK
                                                                                                                                                                                                                                                                                                                                                                  HADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRSRLWSGGAYDSDTEDPDSLK
                       -DRKPIPSRVKREAVEPDTKDKDG-----LKGIMERGKGCEVEVDESGST 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             521 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1496.5; DB Pred. No. 4e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B0F6503D42A1BA32
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                 QEDGDKRWDPDSD-MDVDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                        103;
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RA Becson K.Y. Benos P.V. Berman B.P. Bhandari D. Bolshakov S.
RA Borkova D., Botchan M.R. Bouck J. Brokstein P., Bolshakov S.
RA Borkova D., Botchan M.R. Bouck J. Brokstein P., Bolshakov S.
RA Burtis K.C. Busam D.A. Butler H. Cadieu E. Center A. Chandra I.,
RA Cherry J.M. Cawley S. Dahlke C. Davenport L.B. Davies P.,
RA Cherry J.M. Cawley S. Dahlke C. Davenport L.B. Davies P.,
RA Dodson K., Doup L.E. Downes M. Dugan-Rocha S., Dunkov B.C. Dunn P.,
RA Dodson K., Doup L.E. Downes M. Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Devangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Her M.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Her M., Glasser K.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Moyd A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q. A.,
RA Globs R.A., Myers E.W., Rubin G.M., Venter E., Wang A.H., Wang X.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.*;
DR RHEIL ADDOXABS, Hard Agacetylse.
                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Mohril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Phillippe B., Philippe B., Phi
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Bukaryota: Metazoa: Arthropoda; Tencheata: Hexapoda: Insecta;

Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae: Drosophila.
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Ol-WAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-UN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VZA1
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                                                                                                                       Local Similarity
                         76 HADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHG 135
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                                                                                       KKRYCYYYDSDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATADEMTKF
PF00850; Hist_deacetyl;
S; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                            521 AA;
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56.3%;
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90;
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                                                                                                                                                                                                                                                                           Score 1496.5;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                  wliquet V., Chavez M., Korbers R., Geerts A.;
"Expression pattern of rat histone deacetylases.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF321131; AAK11184.1;
SEQUENCE 428 AA; 48829 MW; 7CB448CFE33041FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                              LTDRVMTVSFHKYGNYFFPGTGDMYEVGAESGRYYCLNVPLRDGIDDQSYKHLFQPVISQ
                                                                                 ATDRVMTVSFHKFGDY-FPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK
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                                                                                                                                                                                                                                                          KTVAYFYDPDVGNFHYGAGHPMKPHRLALTHSLVLHYGLYKKMIVFKPYQASQHDMCRFH
                                                                                                                                                                                                                                                                                          RKYCYFYDPEYGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRFH
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VVDFYQPXCIVLQCGADSLGCDRLGCFNLSIRGHGECVEYVKSFNIPLLVLGGGGYTVRN
                              VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTIRN
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of two putative histone Aspergillus nidulans."; Biochim. Biophys. Acta 1492:120-126(2000).
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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           NMDNANTREYLDKIRTQVVENLKRTAFAPSVQMTDVPRE---
                                                       NMENKNSROMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDS
                                                                                                                 KSFNLPTLIVGGGGYTMRNVARTWAFETGILVGDNLGSELPYNDYYEYFAPDYELDVRPS
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                                                                                                                                                                                                                                                                          DDGIDDESYHLLFKPINGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFM
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Best Local Similarity
Matches 239; Conserv
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Q9JM08;
Q1-OCT-2000 (
Q1-OCT-2000 (
Q1-JUN-2001 (
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Mol. Cell Biol. Res. Commun. 2:91-96(1999).
EMBL; AF098295; AAF28798.1; -.
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MEDLINE=20391214; PubMed=10542131;
Dangond F., Foerznler D., Weremowicz S., Morton C.C.,
Gullans S.R.;
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FENLKMLNHAPSVQIHDVPADLLTYDRTDEADAEERGPEENYSRPEAPNEFYDGDHDNUK
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Rodentia;
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56.1%; Pred. No. 1.8e-98;
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Last annotation updat
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Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
SEQUENCE 428 AA; 48737 MW; EDE9F
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Mammalia; Eutheria;
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Tsai S.C., Kahle E
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"Isolation and characterization
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74; Mismatches
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Query Match
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                     062339 PRELIMINARY; PRT; 46: 062339; 062343; 01-AUG-1998 (TREMBLrel. 07, Created) 01-NOV-1998 (TREMBLREL. 08, Last sequence of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPBC36.05C OR CLR6.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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01-JUN-2001 (TrEMBLrel.
HISTONE DEACETYLASE.
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Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
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Grewal S.I., Bonaduce M.J., Klar A.J.;
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Moestl D., Duesterhoeft A.;
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Pred. No. 1.1e
52; Mismatches
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EMBL; 281108; CAB03240.1; -
EMBL; 281106; CAB03240.1; J
EMBL; 281106; CAB03224.1; -
EMBL; 281106; CAB03224.1; -
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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                              PSRVKREAVEPDTKDKDGLK 447
                                                              LENLKQLPHVPSVQMQSISTSCDSIVKTFDEKLIRDHQNDDVRVTQFEEDVQVED
                                                                                              LHNLSKLQHAPSVPFQ--ERPPDTETPEVDE----DQEDGDKRWDP-DSDMDVDDDRKPI
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                                                                                                                              VSRCWLYETAIALNQEVSDDLPLHDYFDYFIPDYKLHIKPLAALSNFNTPEFIDQTIVAL
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-SAEFYDGQEPETKNIQSMK
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Q9C1C6;
Q1-JUN-2001
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Q1-JUN-2001
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"HDC2, a histone deacetylase gene related to RPD3, from filamentous fungus Cochliobolus carbonum.";
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF349677; AAK35180.1; -.
SEQUENCE 648 AA; 70940 MW; 242147C293D4EAD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cochliobolus carbonum (Bipolaris zeicola).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
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Search completed: April 26, 2002, 17:57:27 Job time: 355 sec

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SEQUENCE FROM N.A.  STRAIN-CY. COLUMBIA;  TOMINAMA T., Shoji K., Hanyu H., Okano T.;  Tominama T., Shoji K., Hanyu H., Okano T.;  Tominama T., Shoji K., Hanyu H., Okano T.;  Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.  -i. FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).  HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).  -i. SUBCILIDIAR LOCATION: NUCLEAR (BY SIMILARITY).  -i. SUBCILIDIAR LOCATION: NUCLEAR (BY SIMILARITY).  -i. SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA FAMILY. HD SUBFAMILY 1.	STANDARD; PRT; 501 AA.  (Rel. 36, Created) (Rel. 36, Last sequence update) (Rel. 40, Last annotation update) ETYLASE (HD). ETYLASE (HD). iridiplantae; Streptophyta; Embryophyta; Tracheophyta; iridiplantae; Streptophyta; eudicotyledons; core eudicots; Rosidae; Brassicales; Brassicaceae; Arabidopsis.	YLFN_CAEEL YB94_METTH YB94_METTH YB94_METTH Y35_METJA Y245_SYNY3 APHA_MYCRA APHA_MYCRA HOS3_YEAST ANK1_MOUSE HIBN_XENLA CYLF_BOVIN SEC7_YEAST YGX7_YEAST YGX7_YEAST ALIGNMENTS Q0295 caecharomyc P06180 xenopus lae CYLF_BOVIN P16039 gallus gall P1075 saccharomyc P53076 saccharomyc

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Pfam; PF00850; Hist\_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE. Hydrolase; SEQUENCE EMBL; AF014824; AAB66486.1; -Nuclear protein. 501 AA; 56037 MW; C50AF5624958D6C2 CRC64;

Ş 밁 Matches Query Match Best Local 61 61 VLKPFPARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQT 120  $\vdash$ 1 MDTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQ VLKPFPARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQT MDTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQ 501; Similarity 100.0%; ilarity 100.0%; Conservative 0 0; Score 2722; DB 1; Pred. No. 1.2e-203; Mismatches 0 Length 501; Indels 0; Gaps 60 60

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Submitted (DEC-1997) to the EMBL/Genbank/DDBJ databases.
-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE UNITERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
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Hydrolase;
SEQUENCE
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Best Local :
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| HDA1_MOUSE | STAN

| 009106; p97476;

| 01-NOV-1997 (Rel. 3

| 01-NOV-1997 (Rel. 3

| 20-AUG-2001 (Rel. 4
                                                                                                                                                                            TISSUE-Fibroblast;
MEDLINE-97415582; PubMed-9271381;
Bartl S., Taplick J., Lagger G.,
                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
20-AUG-2001 (Rel. 40,
HISTONE DEACETYLASE 1
                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                              Johnson C.A.;
Submitted (SEP-1997)
-!- FUNCTION: RESPONS
                                                                                                                                                                                                                                                                                         HDAC1
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                          inducible gene.";
Mol. Cell. Biol.
                                                                                                                                                                  "Identification of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                             482
                                                                                                                                                                                                                                                                                                                                                                                                                                                     471
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FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4). HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).

FUNCTION: ACTS AS A TRANSCRIPTIONAL REPRESSOR SUBUNIT: FORMS A COMPLEY LATT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 YRPNPARERELCRFHAEEYINFLRSVTPETQQDQIRLLKRFNVGEECPVLDGLYSFCQTY
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377; Conser
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                                                                                                                                                                                                                                                        (Mouse).
Chordata;
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                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                           :5033-5043(1997).
                                                                                                                                                                                                                                                      Rodentia;
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75.2%;
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Pred. No. 1.3e
44; Mismatches
                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                 deacetylase
                                                                                                                                                                              Khier H.,
                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                  growth factor
                                                                                                                                                                               Seiser C.;
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RESULT 4
HDA1_HUMAN
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Best Local
HDA1_HUMAN STANDARD;
Q13547; Q92534;
Q1-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00850; Hist_deacetyl;
PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Nuclear protein. SEQUENCE 482 AA; 55075 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X98207; CAA66870.1; -. EMBL; U80780; AAB68398.1; -. MGD; MGI:108086; Hdac1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEX WITH SIN3 AND SAP18 (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHER LEVELS IN THYMUS
AND TESTIS AND LOWER LEVELS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: BY INTERLEUKIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEE 193
                                                                                                                                                                 VGVEEASVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                      GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTKRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMT 65
                                                                                                                                                                                                    EGEGGRKNSSNFKKAKRVKTE----DEKEKD-----PEEKK----EVTEEEKTKEEKPEA 472
                                                                                                                                                                                                                            DVDDDRKPIPS----RVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNP
                                                                                                                                                                                                                                                                                                            LLHNLSKLQHAPSVPFQERPPDTETPEV-DEDQEDGDKRWD------PDSDM 418
                                                                                                                                                                                                                                                                                                                                             RNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQR 365
                                                                                                                                                                                                                                                                                                                                                                  RNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRND 373
                                                                                                                                                                                                                                                                                                                                                                                                                      SKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKPVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVEE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REHADDYVSELRSITPETQQDQIRQLKRENVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
                                                                                                                               KGVKE-EVKL 481
                                                                                                                                                                                                                                                                           LFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEEDPDKRISICSSDKRIACEEEFSDSDE
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60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1554; DB 1
Pred. No. 4.3e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7F64D3C17F5E4844 CRC64;
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                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPD3, a transcription factor in Saccharomyces cerevisiae.";
Cytogenet. Cell Genet. 73:130-133(1996).
-!- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF
THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDAC1 OR RPD3L1.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, 20-AUG-2001 (Rel. 40, HISTONE DEACETYLASE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          Hydrolase; Nuclear protein. CONFLICT 312 312
                                                                                                                                                                                                                                                                                                                        Pfam; PF00850; Hist_deacetyl; PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U50079; AAC50475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
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MEDLINE=96244606; PubMed=8646880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulator Rpd3p.";
Science 272:408-411(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                             MIM; 601241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Akiyama T., Nakamura Y.;
"Isolation and mapping of a human gene (RPD3L1) that is homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Furukawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96185499; PubMed-8602529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A mammalian histone deacetylase related
               134
                                                 66
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                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS. SUBBUIT: FORMS A COMPLEX WITH RBAP48 AND ALSO WITH THE HISTONE ACETYLTRANSFERASE P/CAF AND THE ADAPTATOR PROTEIN P300. ALSO P(A COMPLEX WITH SIN3 AND SAP18. INTERACTS WITH TGIF. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHER LEVELS IN HEART, PANCEAS AND TESTIS, AND LOWER LEVELS IN KIDNEY AND BRAIN. SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA FAMILY. HD SUBFAMILY 1.
                                                                                                               HGLCDIAINWAGGLHHAKKCEASGFCYYNDIVLAILELLKQHERVLYYDIDIHHGDGVEE
                                               KYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLN
                                                                               RFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
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                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                        482 AA;
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.A., Schreiber S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ormatics Institute. There are no resinstitutions as long as its content
                                                                                                                                                                                                                                                                          55103 MW;
                                                                                                                                                                                                   56.7%; Score 1544; DB 1; 59.4%; Pred. No. 2.6e-112;
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Last annotation updat
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4; 4D35B7C1ED7838D6
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P56517;
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Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updath
HISTONE DEACETYLASE 1 (HD1).
                            InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                   EMBL; AF039751; AAB96923.1; -. EMBL; AF043328; AAB99850.1; -.
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1998)
                                                                                                                       EMBL; AF044169; AAC00504.1; -
                                                                                                                                                                                                                                                                        entities requires a
                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
SUBUNIT: FORMS A COMPLEX WITH RBAP48 (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nitted (FEB-1998) to the EMBI/GenBank/DDBJ databases. FUNCTION: RESPONSIBLE FOR THE DEACET/LATION OF LYSINE RESIDUES OF THE HISTONES (HZA, HZB, H3 AND H4). HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY, HD SUBFAMILY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGULATION, CELL CYCLE PROGRESSION
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                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                 Bioinformatics Institute. There are no rest-
profit institutions as long as its content
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Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davie J.R.;
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Best Local Similarity
                                                                                                                                                                                                                 _XENLA
_XENLA STANDARD; PRT; 480 AA.
H012_TXENLA STANDARD; PRT; 480 AA.
042227;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE HISTONE DEACETYLASE 1-2 (HD1) (RPD3)
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PARTERION D., WOLFFE A.P.;

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

SUBMITTON: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).

SIMILARITY: BELLOUGS TO THE HISTONE DEACETYLASE / ACUC / APHA
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                            NCBI_Tax1D=8355;
                                                                                                                                                                                        Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                           Xenopodinae;
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Q91695;
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                                                                                                                                                                                         HISTONE DEACETYLASE) (HDM) (AB21). Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-Aug-2001 (Rel. 40, Last annotation update)
PROBABLE HISTONE DEACETYLASE 1-1 (HD1) (MATERNALLY-EXPRESSED
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                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.6e-110;
77; Mismatches 95;
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"Xenopus HDm, a maternally expressed histone deacetylase, belongs to an another family of acetyl metabolizing enzymes.";

Gene 198:275-280(1997).

1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE UNITERMINAL PARY OF THE CORE HISTONES (HZA, HZB, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

TISSUE SPECIFICITY: OOCYTE.

TISSUE SPECIFICITY: OOCYTE.

DEVELOPMENTAL STAGE: ACCUMULATES IN PREVITELLOGENIC OOCYTES AND I
DEVELOPMENTAL STAGE: ACCUMULATES IN PREVITELLOGENIC OOCYTES AND INTO EARLY
MAINTAINED AT CONSTANT LEVEL THROUGH GASTROLA TO NEUROLA. NOT
EMBRYOGENESIS. DECLINES THROUGH GASTROLA TO NEUROLA. NOT
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SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC
FAMILY. HD SUBFAMILY 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
                                                                                                                                                                                       SKYMEMFQPSAVVLQCGADSLSGDRLGCFNLTIKGHAKCYEFIKTFNLPLLMLGGGGYTI
                                                                                                                                                                                                                                                                                                     AFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTKKKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIFRPHKASAEDMT 65
                                                                                                                                                                                                                             GXVMETERPGAVVLQCGADSLSGDRLGCFNLSTKGHAECVKFMRSFNVPLLLLGGGGYTT
                                                                                                                                                                                                                                                                 AFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYALRDGIDDESYEAIFKPVM
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                                     LFENLRMLPHAPGVQMQAVAEDSIHDDSGEEDEDDPDKRISIRSSDKRIACDEEFSDSED
                                                                                                               RNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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RKP1PS--RVKREAVEPDTKDKDGLKGIMERGKGCEVEVD
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59.88;
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Pred. No. 1.9e-110;
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Matches
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"Transcriptional repression by YY1 is mediated by interaction with a mammalian homolog of the yeast global regulator RPD3.";
Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).
-1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N.-TERMINAL PART OF THE CORE HISTONES (H2A. H2B. H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97075080; PubMed-8917507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN).
HDAC2 OR YY1BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HISTONE DEACETYLASE 2 (HD2) (YY1 TRANSCRIPTION FACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00850; Hist_deacetyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U31758; AAC52889.1; ..
MGD; MGI:1097691; Hdac2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                    SEQUENCE
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DOMAIN 300 303
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                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000286; His_deacetylse
                                  121
                                                                                              61 TAEEMTKYHSDEYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVA 120
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                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                   ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR SIMILARITY: BELONGS TO THE HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: FORMS TRANSCRIPTIONAL REPRESSOR COMPLEXES BY AT LEAST WITH THE ZINC-FINGER TRANSCRIPTION FACTOR YYL. SUBUNIT: FORMS A HETEROLOGOUS COMPLEX WITH YYL.
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GDGVEEAFYATORVMTVSFHKFGDYFPGTGH1QD1GYGSGKYYSLNVPLDDG1DDESYHL
                                                 GSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS
                              GAVKLNRQQTDMAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHH
                                                                                                                    RERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVG
                                                                                                                                                                                                 LASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPA
                                                                                                                                                                MAYSQGGGKKKVCYYYDGDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKA 60
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                                                                                                                                                                                                                                                                                                                    55302 MW;
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                                                                                                                                                                                                                                                 Score 1513.5;
Pred. No. 6.1
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Sciurognathi; Muridae; Murinae; Mus
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GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC

Matches Query Match Best Local

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Conservative

Similarity

55.48;

Score 1507; Di Pred. No. 2.4e 75; Mismatches

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15-JUL-1998
20-AUG-2001
                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE UNITED THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
 Hydrolase;
SEQUENCE
                               PRINTS: PR01270; HDASUPER. PRINTS: PR01271; HISDACETLASE
                                                             InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus (Purple sea urchin) Eukaryota; Metazoa; Echinodermata; Eleutherozoa; I
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                                                                                                EMBL; AF032919; AAB87685.1; -
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Nuclear protein.
576 AA; 64078 MW;
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(Rel. 36, Last sequence up
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RESULT 10
HDA2_HUMAN
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15-JUL-1998
20-AUG-2001
HISTONE DEAC
                                                                                                                                                                                     WEDLINE-97075080; PubMed-8917507;

Yang W.-M., Irouye C.J., Zeng Y., Bearss D., Seto E.;

"Transcriptional repression by YY1 is mediated by interaction with a mammalian homolog of the yeast global regulator RPD3.";

Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).

-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                          HDAC2.
Homo sapiens (Human).
Chordata;
This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                        TISSUE-Breast;
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                                                                                                         FUNCTION: FORMS TRANSCRIPTIONAL REPRESSOR COMPLEXES BY ASSOCIATING WITH MAD, SIN3, YYI AND N-COR.
SUBUNIT: FORMS A HETERCLOGOUS COMPLEX AT LEAST WITH YYI.
SUBCELLULAR LOCATION: NUCLEAR.
                                                       LUNG.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
                                             FAMILY.
                                                                                          TISSUE SPECIFICITY: WIDELY EXPRESSED; LOWER LEVEL IN BRAIN AND
                                                                                                                                                                           SIMILARITY).
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1998 (Rel. 36, Last sequence update)
2001 (Rel. 40, Last annotation update)
DEACETYLASE 2 (HD2).
                                             HD SUBFAMILY 1.
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the Swiss Institute of Bioinformatics

and the

EMBL outstation

Ephydroidea; Drosophilidae; Drosophila. NCBI\_TaxID-7227;

Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Ho Pterygota; Neoptera; Endopterygota; Diptera;

Hexapoda; Insecta;

Brachycera;

Muscomorpha

update)

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RESULT 11

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ID HDAC_LE
ID 40AC_1E
AC Q94517
AC Q94517
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DT 15-JUL
DT 15-JUL
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Best Local S
Matches 277
                                                                                     HDAC_DROME STANDARD: PRT; 520 AA Q94517; 017429; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) PROBABLE HISTONE DEACETYLASE (HD) (DRPD3). RRD3 OR HDAC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00850; Hist_deacetyl; PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE
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CONFLICT
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PRINTS; PR01271; HISDACETLASE.
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InterPro; IPR000286; His_deacetylse.
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"The histone deacetylase RPD3 counteracts genomic silencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y09258; CAA70455.1; -. EMBL; AF026949; AAC23917.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97113416; PubMed-8955276;
245 VMETFQPAAVVLQCGADSLTGDRLGCFNLTVKGHGKCVEFVKKYNLPFLMVGGGGYTIRK
                                                          185
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                                                                                                                                                                                                          76
                                                                                                                                                                                                                                                                   16 KRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rubertis F., Kadosh D., Henchoz S., Pauli D., Reuter G., Struhl K.,
                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nson C.A., White D., O'Neill L.P., Turner B.M.;
mitted (NOV-1997) to the EMBL/GenBank/DOBJ databases.
FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
SIMILARITY). IN DROSOPHILA, IT IS INVOLVED IN POSITION-EFFECT
VARIEGATION (PEV) AND IS DIRECTLY INVOLVED IN COUNTERACTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENOME SILENCING
                             VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGGYTIRN
                                                       YATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK 255
                                                                                                                                                                                             HADDYVSFLRSITPETQQDQIRQLKRENVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHG 135
                                                                                                                     ASEICINWGGGLHHAKKSEASGFCYVNDIVLGILELLKYHQRVLYIDIDVHHGDGVEEAF
                                                                                                                                                 LCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAF 195
                                                                                                                                                                            HCDEYVRFLRSIRPDNMSEYNKQMQRFNVGEDCPVFDGLYEFCQLSAGGSVAAAVKLNKQ 124
                                                                                                                                                                                                                                         KKRVCYYYDSDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMDI-RPHKATADEMTKF
                                                                                                                                                                                                                                                                                                  al Similarity
267; Conserv
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Pred. No. 3
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D -> N (IN REF 2).
E -> D (IN REF 2).
V -> VV (IN REF 2).
L -> V (IN REF 2).
S -> T (IN REF 2).
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                                                                                                                                                                                                                                                                                                  Mismatches 105;
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                                                                                                                                                                                                                                                                                                                .7e-107;
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-I: FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE UNITED ACTIVATION OF LYSINE RESIDUES OF THE UNITED ACTIVATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
HISTONE DEACETYLASE 2 (HD2).
                                                                                                                                                                                                                                                                                                            PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus
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15-JUL-1998
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDA2_CHICK
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO
Pfam; PF00850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                               Hydrolase; Nuclear
 121
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                                                                                                                                                                                       Local Similarity
nes 274; Conser
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SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL)
SIMILARITY: BELONGS TO THE HISTONE DEACET
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EGGRRDNRSYKGQRKRPRLDKDTNSNKASSETSSEIKDEKEKGDGADGEESTASNT 480
                            GSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHH 187
                                                                                                                        LASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPA
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                                                             TAEEMTKYHSDEYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVA
                                                                                          RERDLCREHADDYVSFLRSITPETQQDQIRQLKRENVGEDCPVFDGLYSFCQTYAGGSVG 127
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                                                                                                                                                                                                                                                                                                                                                           IPR000286; His_deacetylse
                                                                                                                                                                                                                                                                  488 AA;
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                  55153 MW; 4F79B9C0D4A2D065 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                    53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO THE HISTONE DEACETYLASE / ACUC / APHA
                                                                                                                                                                                       81;
                                                                                                                                                                                                    Score 1465.5; DB 1
Pred. No. 3.2e-106;
                                                                                                                                                                                                                                                                                   POLY-GLY.
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                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                       Indels
                                                                                                                                                                                                                    Length 488;
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or send a
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15-JUL-1998 (Rel. 36, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
PROBABLE HISTONE DEACETYLASE 1.
HDA-1 OR C53A5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                        EMBL; Z81486; CAB03984.1; -. WormPep; C55A5.3; CE08992. InterPro; IPR000286; His_deacetylse. Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (HZA, HZB, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                    PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY) SIMILARITY: BELONGS TO THE HISTONE DEACETYLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
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                                                                                                                         Nuclear protein.
461 AA; 52137 M
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57.2%;
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      Score 1392; DB 1;
Pred. No. 1.5e-100;
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P56520;
15-JUL-1998
                                               use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                        CHICK
                         EMBL;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves;
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20-AUG-2001
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                                                                                                                                                                    SIMILARITY).
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                           FAMILY. HD
                                                                                                                                                                                                             REGULATION, CELL CYCLE
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                       AF039753; AAB96925.1; -
         IPR000286; His_deacetylse
                                                                                                                                                                                                                                                                                                                                                            Metazoa;
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(Rel. 40, Last annotation
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                                                                                                                                                           SUBFAMILY 1
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                                                                                                                                                                                                                                                                                                                                                Neognathae;
                                                                                                                                                                                                                                                                                                                                                            Chordata;
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                                                                                                                                                                                     NUCLEAR
                                                                                                                                                                                                              PROGRESSION
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                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
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                                                             (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                            HDA3_HUMAN STANDARD; PRT; 428 AA. 015379; 043268; 09UEV0; 09UEI5; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 20 AUG-2001 (Rel. 40, Last annotation update) HISTONE DEACETYLASE 3 (HD3) (RPD3-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
additional member of the human histone deacetylase gene family."; J. Biol. Chem. 272:28001-28007(1997).
                                                                                                                             "Differential display cloning of a novel human histone (HDAC3) cDNA from PHA-activated immune cells."; Blochem. Blophys. Res. Commun. 242:648-652(1998).
                                                                                                                                                                            Dangond F., Hafler D.A., Tong J.K.,
Gullans S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
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                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND TISSUE-Fibroblast;
                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-T-cell, and Spleen;
MEDLINE-98125547; PubMed-9464271;
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                            Yang W.-M., Yao Y.-L., Sun J.-M., Davie J.R., Seto E.: "Isolation and characterization of cDNAs corresponding to
                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                MEDLINE-98010646;
                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATDRVMTVSFHKFGDY-FPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFY 196
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428 AA; 48901 MW; 42E32733AD2BBF07 CRC64;
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                                                                 PubMed-9346952;
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                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                2).
                                                                                                                                                                                             Randall J., Kojima R., Utku N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88;
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SEDYIDFLQRVSPTNMQGFTKSLNAFNVGDDCPVFPGLFEFCSRYTGASLQGATQLNNKI

ADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGL 136 : | ||||:||:|| : || |||||||:|: || : ||:|: || : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

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SEQUENCE FROM N.A. (ISOFUMM 1, SEQ
  Matches
                              Best
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                              EMBL: U66914; AAC52038.1; -.
EMBL: U75697; AAB88241.1; -.
EMBL: U75696; AAB88240.1; -.
EMBL: AF005482; AAB87752.1; -.
EMBL: AF039703; AAC98927.1; -.
EMBL: AF059650; AAC26509.1; -.
EMBL: AF053138; AAC08351.1; -.
EMBL: AF053138; AAC08351.1; -.
EMBL: AF053139; AAC08352.1; -.
                                                                                                                                  CONFLICT
SEQUENCE
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[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatis the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annouentities requires all license agreement (See http://www.isb-sib.ch/annouentities requires all license agreement (See http://www.isb-sib.ch/annouentities requires all license agreement (See http://www.isb-sib.ch/annouentities agreementities 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -II- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (42A, 42B, 43 AND 44).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS.

-II- FUNCTION: MAY PARTICIPATE TO THE REGULATION OF TRANSCRIPTION THROUGH ITS BINDING MITH THE ZINC-FINGER TRANSCRIPTION FACTOR YYLLINCREASES YYL REPRESSION ACTIVITY.

-II- SUBBURIT: FORMS A HETERNOLOGOUS COMPLEX AT LEAST WITH YYL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-99162406; PubMed-10051405;
Mahlknecht U., Emillani S., Najfeld V., Young S., V
"Genomic organization and chromosomal localization
histone deacetylase 3 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lynch E.D., Lee M.K., King M.-C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   histone deacetylase 3 gene
Genomics 56:197-202(1999).
                                                                                                                                                                                                                                                                    PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                             MIM; 605166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 95-353 AND 407-428 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                    InterPro;
                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/RPD3-2B (SHOWN HERE)
2/RPD3-2A: ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC FAMILY. HD SUBFAMILY 1.
                           Similarity
                                                                                                                                                                                                                                                                                                                                                    IPR000286; His_deacetylse
                                                                                                                         359
428
                                                                                                                                                                                                                                              Nuclear
  Conservative
                                                                                                                                    <u>₹</u>
                                                                                                                                                                                                                                                                                                                      Hist_deacetyl;
                                                                                                                                                                                                                                        protein; Alternative splicing
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                                                                                                                                                                                                                  15
                                                                                                                                    48847
                           56.6%;
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  73;
                                                                                                                               ISOFORM 2).
R -> L (IN REF. 1)
; 94485C1EBDCF5AD0
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RPD3 ortholog, HDAC3
                                                    Score
                           Pred.
                                                                                                                                                                                                                  MAKTVAYFYDPDVGN -> MIVFKPYQASQHDMCR (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95:2795-2800(1998).
Mismatches
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(See http://www.isb-sib.ch/announce/
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  90;
                                                                                                                                    CRC64;
                                                    Length
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  22;
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Gaps
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Search completed: April 26, 2002, 17:57:50 Job time: 333 sec

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Maximum DB seq length: 2000000000
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Perfect score:
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    1167-98
1107-5
1066-5
471-47-6
448-5
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2722
1 MDTGGNSLASGPDG
    April 26, 2002, 17:50:57; Search time 25.88 Seconds (without alignments) 1474.631 Million cell updates/sec
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Com
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Result No.

275.5 10.1 1095 2 T13964 271.5 10.0 338 2 H84173 264 9.7 335 1 H71071 261.5 9.6 310 2 H27050 243.5 8.9 796 2 T32425 238 8.7 331 1 C69026 236 8.7 517 2 T27101 230.5 8.5 38.5 2 A81926 230. 8.4 34.3 1 C64366 227 8.3 306 2 D82126 227 8.3 306 2 D82126 224.5 8.2 369 2 F81178 223.5 8.2 359 2 T05998 208 7.6 304 1 \$7457 201 7.4 301 2 H75470 197 7.2 346 2 H83605
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## ALIGNMENTS

RESULT T05640

Wayer,
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A;Gene: rpd3
C;Superfamily: RPD3 protein; RPD3/acuC homology
C;Keywords: hydrolase
F;27-325/Domain: RPD3/acuC homology <RAH>
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A;Residues: 1-513 <ROS>
A;Cross-references: EMBL:AF035815; NID:g2665839; PIDN:AAC50038.1;
A;Experimental source: strain W22
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Gen. Genet. 258, 288-296, 1998
A; Title: Identification and characterisation of an RPD3
A; Reference number: 214321; MUID:98307342
A; Accession: T01413
A; Accession: T01413
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                                         DHKAVEESSRRSILGIKIKREFGENATRVQDGGR-VASEHRGLEPMAEDIGSSKQAPQAD 48.
                                                                                                                    NSRQMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVD
                                                                                                                                                                               PLLLLGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENK
                                                                                                                                                                                                                                                                                     DIDIHHGDGVEEAFYTTDRVMTVSFHKFGDYFPGTGDIRDIGHSKGKYYSLNVPLDDGID
                                                                                                                                                                                                                                                                                                                                                                                                                                       LKPFPARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGNSLAS-GPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQV
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                                                                     DD-----RKPIPSRVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTK---VTG
                                                                                                     NTROOLDDIRS----KLSKLRHAPSVHFQERVPDTEIPEQDEDQDDPDERHDPDSDMEVD
                                                                                                                                                                                                                                                                                                                                                   AGASVGGAVKFNHG-HDIAINWSGGLHHAKKCEASGFCYVNDIVLAILELLKHHERVLYV
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                                                                                                                                                                 PLLLLGGGGYTIRNVARCWCYETGVALGQEPEDKMPVNEYYEYFGPDYTLHVAPSNMENK
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75.2%;
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RPD3 protein homolog - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999
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                     A; Molecule type: DNA
A; Residues: 1-461 <WIL>
                                                                                                               submitted to the EMBL Data Library, A; Reference number: 219232
                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 31-Jan-2000
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A; Residues: 1-480 <LAD>
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A; Accession: $60381
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R;Ladomery, M.R.; Lyons, S.; Sommerville, J.
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A;Cross-references: EMBL:Z81486; PIDN:CAB03984.1; GSPDB:GN00023;
                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                        A; Accession: T20163
                                                                                                                                                               R; Mortimore,
                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                                                                         hypothetical protein C53A5.3 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLHNLSKLQHAPSVPFQERPPDT ---ETPEVDEDQED-----GDKRWDPDSDMDVDDD 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEE1KND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFYATDRYMTYSFHKFGDYFPGTGHIQDIGYGSGKYYSLNYPLDDGIDDESYHLLFKPIM 253
                                                                                                                                                                                                                                                                                                                                                                         EGEGGRKNVANFKKVKRVKTE-EEKEGEDKKDVKEEEKAKDEKTD
                                                                                                                                                                                                                                                                                                                                                                                                                    ----RKPIPS--RVKREAVEPDTKDKDGLKGIMERGKGCEVEVD 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFENLRMLPHAPGVQMQAVAEDSIHDDSGEEDEDDPDKRISIRSSDKRIACDEEFSDSED
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Pred. No. 6.8e-110;
                                                                                                                                            November
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CESP:C53A5
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A:Introns: 19/1; 46/3; 94/2; 121/3; 140/3; 159/2; C;Superfamily: RPD3 protein; RPD3/cacuC homology C:Keywords: hydrolase; phosphoprotein F;7-307/Domain: RPD3/cacuC homology  RRH1> F;232,282,404/Binding site: phosphate (Tyr) (coval)
                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AF074881
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Mahlknecht, U.; Hoelzer, D.; Bucala, R.; Verdin, E. Blochem. Blophys. Res. Commun. 263, 482-490, 1999 A:Title: Cloning and characterization of the murine h. A:Reference number: JC7102; MUID:99423490 A:Accession: JC7102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histone deacetylase (EC 3.5.1.-) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
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A; Introns: 58/3; 98/1;
C; Superfamily: RPD3 pro
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A; Residues: 1-424 <MAH>
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                                                                                                                                                       :232,282,404/Binding site: phosphate (Tyr) (covalent)
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                                                    Query Match
Best Local Similarity
                                 Matches
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                      Score 1366; DB 2,
Pred. No. 4.8e-98;
"'amatches 91;
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                                                                                                                                                                                                                                                                  204/1; 231/1; 252/3; 277/2; 307/2;
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                                                                             Length 424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C: Accession: JC5834
C: Accession: JC5834
R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R:Dangond, R:Dangond,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blochem. Blophys. Res. Commun. 242, 648-652, 1998
A;Title: Differential display cloning of a novel human histone
A;Reference number: JC5834; MUID:98125547
A;Accession: JC5834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           histone deacetylase (EC 3.5.1.-) 3 - human
C;Species: Homo sapiens (man)
C;Date: 05-Mar-1998 *sequence_revision 13-Mar-1998 *text_change 12-Nov-1999
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A; Residues: 1-428 < DAN>
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Best Local S
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                                                                                                                                                          SEDYIDFLQRVSPTNMQGFTKSLNAFNVGDDCPVFPGLFEFCSRYTGASLQGATQLNNKI 122
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d gene for a putative aryi-alcohol dehydrogenase. A; Reference number: S57391; MUID:96021610 A; Accession: S57393
                                                                                                                                                                                                   A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995 R;van Dyck, L.; Pascual-Ahuir, A.; Purnelle, B.; Goffeau, A. Yeast 11, 987-991, 1995
A;Title: An 8.2 kb DNA segment from chromosome XIV carries the RPD3 and PAS8 genes as
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome A;Reference number: S55859; MUID:95373280 A;Accession: S55859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, Jaquary 1995 A;Description: Sequence analysis of a 13.9 Kb fra A;Reference number: S51285 A;Accession: S51285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;van Dyck, L.; Pascual-Ahuir, A.; Goffeau, A. submitted to the EMBL Data Library, December 1994
A;Description: A 8.2 kb DNA segment from chromosome XIV carries the RPD3 and PAS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 23-Mar-2001 C;Accession: S22284; S51336; S51285; S55859; S57393; S63313; S63311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription regulator RPD3 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein NO305; protein YNL330c C;Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-201 <MAF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Maftahi, M.; Nicaud, J.M.; Levesque, Yeast 11, 567-572, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1.201 <NIC>
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A; Residues: 1-433 <VAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         icated gene for a putative aryl-alcohol dehydrogenase
A;Reference number: S51334
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A; Residues: 1-433 <VID>
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   A; Cross-references:
                               A; Residues: 1-433 <VAW>
                                                           A; Molecule type: DNA
                                                                                    A;Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z46259; NID:g633655; PIDN:CAA86368.1; PID:g854536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:246259; NID:g633655; PIDN:CAA86368.1; PID:g854536
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;Accession: S22200;
;Vidal, M.; Gaber, R.F.
;Vidal, M.; Gaber, R.F.
;All Gall, Biol. 11, 6317-6327, 1991
;All Gall, Biol. 11, 6317-6327, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Saccharomyces cerevisiae
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EMBL: X83226; NID: 9642335;
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PIDN:CAA58228.1; PID:g642338
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C;Superfamily: RPD3 protein; RPD3/acuC homology C;Keywords: nucleus; transcription regulation F;23-322/Domain: RPD3/acuC homology <RAHI>
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R; Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin,
submitted to the Protein Sequence Database, April 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: SGD:S0005274; MIPS:YNL330c A:Map position: 14L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SGD: RPD3; SDI2; SDS6; MIPS: YNL330c
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A; Residues: 1-433 <COS>
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                                                                                                                                                                                                                                                256
                                                                                                                                                                                                                                                                                                 198
                                                                                                                                                                                                                                                                                                                                               196 YATDRVMTVSFHKFGDYFPGTGH1QD1GYGSGKYYSLNVPLDDG1DDESYHLLFKPIMGK
                                                                                                                                                                                                                                                                                                                                                                                                   138
                                                                                                                                             316 VARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRNDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                            136 LCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAF 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 KRKYCYFYDPEYGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                              HNLSKLQHAPSVPFQERPPDTE-TPEVDEDQED-----GDKRWDPDSDMDVDDD 423
                                                                                                                                                                                                                                             VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGGYTIRN 315
                                                                                                                                                                                                                                                                                                                                                                                                   KCDVAVNYAGGLHHAKKSEASGFCYLNDIVLGIIELLRYHPRVLYIDIDVHHGDGVEEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTDEYIDFLSRVTPDNLEMFKRESVKFNVGDDCPVFDGLYEYCSISGGGSMEGAARLNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRRVAYFYDADVGNYAYGAGHPMKPHRIRMAHSLIMNYGLYKKMEIYRAKPATKQEMCQF 77
ANLENTKYAPSVQLNHTPRDAEDLGDVEEDSAEAKDTKGGSQYARDLHVEHDNE
                                                                                               VARTWCFETGLLNNVVLDKDLPYNEYYEYYGPDYKLSVRPSNMFNVNTPEYLDKVMTNIF
                                                                                                                                                                                                 IMEWYQPSAVVLQCGGDSLSGDRLGCFNLSMEGHANCVNYVKSFGIPMMVVGGGGYTMRN
                                                                                                                                                                                                                                                                                                 YTTDRVMTCSFHKYGEFFPGTGELRDIGVGAGKNYAVNVPLRDGIDDATYRSVFEPVIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
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  431
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N;Alternate names: cryptic loci regulator protein clr6 c;Species: Schizosaccharomyces pombe C;Date: 03-Dec:1999 #sequence\_revision 03-Dec:1999 #text\_change 21-Jul-2000 C;Accession: T40300; T43796

histone deacetylase (EC 3.5.1.-) - fission yeast (Schizosaccharomyces pombe) N;Alternate names: cryptic loci regulator protein cir6

T40300

R; Lyne, M.; Wood, V.; Rajandream, M.A.; submitted to the EMBL Data Library, May

Barrell, B.G.; Hilbert, 1998

H.; Moestl, D.;

Duest

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Accession: T40300 A; Reference number: Z21919

```
hypothetical protein R06C1.1 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC:Accession: T23963; T24071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Cross-references: EMBL:AF064206; NID:g4159996; PIDN:AAD05211.1: PID:g4159997 A:Experimental source: strain 972 C:Genetics: A:Gene: clr6; SPBC36.05c A:Gene: clr6; SPBC36.05c A:Map position: A.Map position: 2 A:Introns: 14/1; 34/3; 51/3; 91/1; 101/2; 116/1; 131/2; 209/3; 240/3; 277/1; 3:C:Superfamily: RPD3 protein; RPD3/acuC homology C:Keywords: hydrolase; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: DNA
A:Rolecule type: DNA
A:Residues: 1-405 <LYN>
A:Residues: 1-405 <LYN>
A:Residues: 1-405 <LYN>
A:Residues: EMBL:AL023589; PIDN:CAA19053.1; GSPDB:GN00067; SPDB:SPBC36.05c
A:Bxperimental source: strain 972h; cosmid c36
R:Grewal, S.I.; Bonaduce, M.J.; Klar, A.J.
Genetics 150, 563-576, 1998
A:Title: Histone deacetylase homologs regulate epigenetic inheritance of transcriptional
A:Reference number: 222685; MUID:98429513
A:Recession: T43796
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecules of transcriptional
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submitted to the EMBL Data Library, October 1996
A; Reference number: Z19837
                                                                                                                                                                A; Status: preliminary; translated from
                                                                                                                                                                                                A; Reference number: Z19824
A; Accession: T23963
                                                                                                                                                                                                                                            submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                              R; Kershaw,
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A; Residues: 1-405 <GRE>
                                                 R;Kershaw, J.
                                                                    A;Cross-references: EMBL:Z81106; PIDN:CAB03224.1; GSPDB:GN00019; CESP:R06C1.1
A;Experimental source: clone R06C1
                                                                                                                         A; Residues: 1-465 <WIL>
                                                                                                                                                     A; Molecule
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Best Local Similarity
Matches 235; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 HIMOWFRPEAVILOCGTDSLAGDRLGCFNLSMKGHSMCVDFVKSFNLPMICVGGGGGYTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYATDRYMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHNLSKLQHAPSVPFQERPPD 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVARVWTYETGLLAGEELDENLPYNDYLQYYGPDYKLNVLSNNMENHNTRQYLDSITSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTIR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNAEIAINWAGGLHHAKKREASGFCYVNDIALAALELLKYHQRVLYIDIDVHHGDGVEEF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTDEYIEFLWRYTPDTMEKFQPHQLK-FNYGDDCPYFDGLYEFCSISAGGSIGAAQELNS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HADDYVSFLRSITPETQQD-QIRQLKRENVGEDCPVFDGLYSFCQTYACGSVGGSVKLNH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKKVSYFYDEDVGNYHYGPQHPMKPHRVRMYHNLVVNYNLYEKLNVITPVRATRNDMTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYTTDRVMTCSFHKFGEYFPGTGHIKDTGIGTGKNYAVNVPLRDGIDDESYESVFKPVIS
                                                                                                                                              type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384
                                                                                                                                                                     GB/EMBL/DDBJ
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A; Map position: 3
A; Introns: 47/3; 8;
A; Note: T18B22.80
C; Superfamily: RPD:
                                                                                                                                                                                                                                                                                                      hypothetical protein T18B22.80 - Arabidopsis thaliana C;Speckes: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 *sequence_revision 20-Apr-2000 *text_change 21-Jul-2000 C;Accession: T47443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-465 <WI2>
A;Cross-references: EMBL:Z81108; PIDN:CAB03240.1; GSPDB:GN00019; CESP:R06C1.1
A;Experimental source: clone R09B3
                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-419 < JOR>
                                                                                                                                                                                             A; Accession: T47443
A; Status: preliminary
                                                                                                                                                                                                                                                            R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; submitted to the Protein Sequence Database, February 2000
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
T47443
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A; Introns: 53/3; 212/1; 279/1; 326/1
                                                                                       C; Genetics:
                                                                                                       A;Cross-references: EMBL:AL138652
A;Experimental source: cultivar Columbia; BAC clone
                                                                                                                                                                                                                                          A; Reference number: Z24467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 VMEIFRPGAVVLQCGADSLSGDRLGCENLSIKGHAECVKEWRSENVPLLLLGGGGYTIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 YATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.0%; Score 1334; DB 2; Local Similarity 55.9%; Pred. No. 1.6e-95; hes 246; Conservative 74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSRCWLYETAIALNQEVSDDLPLHDYFDYFIPDYKLHIKPLAALSNFNTPEFIDQTIVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENLKQLPHVPSVQMQSISTSCDSIVKTFDEKLIRDHQNDDVRVTQFEEDVQVED-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTTDRVMTVSFHKHGEYFPGTGDLKDVGAGSGKYYALNVPLRDGVDDVTYERIFRTIMGE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSDDYINFLRNVKSDNMSTFTDQMARFSVGEDCPVFDGMYEFCQLSCGGSLAAAARLNRQ 126
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RPD3 protein; RPD3/acuC homology
                                          87/1; 112/1; 185/2; 206/3; 237/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                        270/1; 286/3; 317/1; 340/3; 373/3;
                                                                                                            T18B22
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135

144

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A:Map position: 1L
C;Function:
A;Description: involved in the meiotic cell cyc.
A;Description: involved in the meiotic cell cyc.
C;Superfamily: RPD3 protein; RPD3/acuC homology
C;Keywords: hydrolase
F;30-330/Domain: RPD3/acuC homology <RAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z22404; MUID:99452937
A;Accession: T43300
A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: T43300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               histone deacetylase (EC 3.5.1.-) - fission yeast (Schizosaccharomyces pombe)
W,Alternate names: Phdl protein
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 **sequence_revision 16-Jul-1999 **text_change 21-Jul-2000
C;Accession: T11643; T43300
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-434 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL021046

R;Kim, Y.B.; Honda, A.; Yoshida, M.; Horinouchi,
FEBS Lett. 436, 193-196, 1998

A;Title: Phdl+, a histone deacetylase gene of Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: 217304
A;Accession: T11643
A;Status: preliminary; translated from GB/EMBL/DDBJ
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    KKRVTYHLDEQVGNYHYGDKHPMKPHRITITNHLVMGYGLHNKMSVFSPRMATEGEMSEF
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                                           KRKYCYFYDPEVGNYYYGOGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRF 75
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4: Mismatches 94;
                                                                                    Score 1167.5; DB 2;
Pred. No. 1.2e-82;
5; Mismatches 120;
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A; Introns: 45/1; 298/2
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A; Residues: 1-507 <WIL>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 228
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                                           LKLFESVISGVEENFNPEAIVLQCGSDSLCEDRLGQFALSFNAHARAVKYVKSLGKPLMV
                                                                     HLLEKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLL
                                                                                                                              HHGDGVQEAFNNSDRVMTVSFHRFGQYFPGSGSIMDKGVGPGKYFAINVPLMAAIRDEPY
                                                                                                                                                   HHGDGVEEAFYATDRVMTVSFHKFGDYFFGTGHIQDIGYGSGKYYSLNVPLDDGIDDESY
                                                                                                                                                                                                                VEGARRLNHKMNDIVINWPGGLHHAKKSEASGFCYVNDIVLGILELLKYHKRVLYIDIDI
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                                                                                                                                                                                                                                                                                                                                                                                                                          PDGV---KRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPAR 68
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46.7%; Pred. No. 1.5e
tive 77; Mismatches
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1.5e-75;
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138

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364

258 245 198 185 432

372

324 314 264 254 204

31-Jan-2000

CESP: C08B11.2

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A; Map position:
C; Superfamily: RI
F; 30-331/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable transcription regulator YGL194c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein G1330 C;Specles: Saccharomyces cerevisiae G;Date: 17-May-1996 *sequence_revisiae C;Date: 17-May-1996 *sequence_revision 17-May-1996 *text_change 20-Jun-2000 C;Accession: S6421; S62051 R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delnosubmitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Molecule type: DNA
A;Restdues: 1-351,'HSGTHS',358,'RIJHFT',365-452 <COG>
A;Cross-references: EMBL:X91837; NID:g1177627; PIDN:CAA62950.1; PID:g1177634
A;Experimental source: strain FY1679
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:272716; NID:g1322818; PIDN:CAA96906.1; PID:g1322819; MIPS:YGL1 A;Experimental source: strain S288C
R;Coglievina, M.; Delneri, D.; Zaccaria, P.; Klima, R.; Bertani, I.; Bruschi, C.V. submitted to the EMBL Data Library, September 1995
A;Description: A 6.7 Kb fragment from chromosome VII of Saccharomyces cerevisiae contains.
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A; Accession: S64211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SGD: HOS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S62051
A; Accession: S62051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: RPD3 protein; RPD3/acuC homology;30-331/Domain: RPD3/acuC homology <RAH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                              137
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                                                                                                                                                                                                                                                                                                                                                                                                                             18 KYCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRFHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLLGGGGYTIRN 315
                                         LIMTEKPTLIVQQCGADSLGHDRLGCFNLNIKAHGECVKFVKSFGLPMLVVGGGGYTPRN
                                                                                                                                                 ATDRVMTVSFHKF-GDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK 255
                                                                                                                                                                                                                                                         CDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFY 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGGGGYTLRNVARCWALETGVILGLRMDDEIPGTSLYSHYFTPRLLRPNLVPKMNDANSA 378
VARCWCYETGVALGVEVEDKMPEH-EYYEYFGPDYTLHVAPSNM-ENKNSRQMLEEIRND 373
                                                                                                                             TTDRVFTLSFHKYNGEFFPGTGDLTEIGCDKGKHFALNVPLEDGIDDDSYINLFKSIVDP 266
                                                                                                                                                                                                                                                                                                                                             DDYVSFLRSITPETQQDQIR-QLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGL 136
                                                                                                                                                                                                                                                                                                                                                                                     RVSYHFNSKVSHYHYGVKHPMKPFRLMLTDHLVSSYGLHKIMDLYETRSATRDELLQFHS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYLASIEKETLACLRMIRGAPSVQMQ----NIVGIRLDEIEQIEENERLQKSSKSSIEYE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDE-DQEDGDKRWDPDSDMDVDDD 423
                                                                                                                                                                                                               SDIAINWSGGLHHAKKNSPSGFCYVNDIVLSILNLLRYHPRILYIDIDLHHGDGVQEAFY
                                                                                                                                                                                                                                                                                                 EDYVNFLSKVSPENANKLPRGTLENFNIGDDCPIFQNLYDYTTLYTGASLDATRKLINNQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1066.5; DB 2; Pred. No. 8.1e-75;
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D70388
A; Reference number: S54059
A; Accession: S54089
A; Molecule type: DNA
A; Residues: 1~470 <BAD>
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                                                                               submitted to the EMBL Data
                                                                                                       R; Badcock, K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-375 < AQF>
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Best Local (
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                                                                                                                                                                                                                                                                                                                     299 PYALARAWTLIWCELSGREVPEKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      VEEPEVYLLQLGTDPLLEDYLSKENLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116;
                                                                                                       Churcher, C.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                               Library,
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hypothetical protein YPR068c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein YP9499.23c C;Species: Saccharomyces cerevisiae
                                                                      C:Date: 08-Jul-1995 *sequence_revision 19-Oct-1995
C:Accession: S54089
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000719; NID:g2983517; PIDN:AAC07100.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acetoin utilization protein - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Superfamily: acetylpolyamine aminohydrolase; RPD3/acuC;6-306/Domain: RPD3/acuC homology <RAHl>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 IRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 ----EAERCQCVPKGAREKYNIGGYENPVSYAMFTGSSLATGSTVQAIEEFLKG--NVAF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 DYGKYRYPKNHPLKIPRVSLLLRFLDAMNLIDEKELIKSRPATKEELLLFHTEDYINTLM 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWAGGLHHAKKCEASGFCYVNDIVLAILELLKQ-HERVLYVDIDIHHGDGVEEAFYATDR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMTVSFHKFGDY-FP-GTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGKVME 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1FRPGAVVLOCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPL------LLLGGGGGYT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFVLSLHQSPEYAFPFEKGFLEEIGEGKGKGYNLNIPLPKGLNDNEFLFALEKSLEIVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLHNLSKLQHAPSVPFQERPPDTE----TPEVDEDQEDGDKRWDPDSDMDVDDDRK 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.5%; Score 475; DB 2; 32.4%; Pred. No. 3.9e-29; tive 67; Mismatches 127
мау 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NVAFLKAFNIVREVFGEGVYLGGGGYH 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127;
                                                                                                             #text_change 06-Feb-1998
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A;Cross-references: EMBL:Z49219; NID:g805025; PID:g805048; MIPS:YPR068c A;Experimental source: strain AB972 C;Genetics: A;Gene: SGD:HOS1 Ş Q 밁 Ş 문 Ş Dр ş DЬ Q DЪ δÃ 몽 A:Cross-references: SGD:S0006272; MIPS:YPR068c A:Map position: 16R C:Superfamily: RPD3/acuC homology F:9-383/Domain: RPD3/acuC homology <RAH1> 당 Ouery Match 17.3%; Score 471.5; DB 2; Length 470; Best Local Similarity 28.6%; Pred. No. 9.9e-29; Matches 128; Conservative 65; Mismatches 133; Indels 121; Gaps 436 YQYWIY----EMEGSSRMKML---RND 455 140 INNSEVPTNDKPTDTYILNSETKQYNLEGDCPIESYLPMYCQVITGATLNLLDHLSPTER 199 316 PLIERHEPEALLIECGGDGLLGDRFNEWQLTIRGLSRIIINIMKSYPRAHIFLLGGGGYN 375 349 --YTLHVAPSNMENKNSROMLEEIRND 373 376 DILMSRFYTYLTWCVTKQFSNLRCGDNNSFQIDPFDVCDGDDSEQFIREHDLVEMYNEEN 435 313 IRNVARCWCYET------348 255 KVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAE-CVKFMRSF-NVPLLLLGGGGYT 312 260 YSKQIQTISVHLYEPGFFPGTGSLSD----SRKDKNVVNIPLKHGCDDNYLELIASKIVN 315 197 ATDRVMTVSFHKF-GDYFPGTGHIQDIGYGSGKYYS-LNVPLDDGIDDESYHLLFKPIMG 254 80 QDVNNPMVESKWSELSELADNWNEKIDYNPSQDLQRFTTRENLYNYYLNHSQALENNMDC 139 85 20 PCNNHQKSQLTYSLINAYDLLQHFDEVLTFPYARKDDLLEFHSKSYIDYLINGRFNKMMA 79 37 PMKPH-RIRMTHALLAHYGLLQHMQYLKPFP-ARERDLCRFHADDYVSFL------ 84 IR------QLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGLC 137 -----RSITPETQQDQ 95 14;

Search completed: April 26, 2002, 17:52:45 Job time: 108 sec

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Minimum DB seq length: U
Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Comp
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Qy 242 DESYHLL                   Db 247 DESYQSL   Qy 302 PLLLLGG	8 SGGN8 62 LKPFFF 62 LKPFFF 11 68 YRPNI 122 AGGSS 11 128 AGASS 182 DIDII 187 DIDII	RESULT 1 US-09-282-305 8 Sequence 8, App Patent No. 6287 GENERAL INFORMA APPLICANT: Ba APPLICANT: Ba APPLICANT: BT TITLE OF INVEN FILE REFERENCE CURRENT APPLICAT PRIOR APPLICAT PRIOR APPLICAT PRIOR APPLICAT PRIOR FILING ON CONTRACT SEQ ID NO 8 SOFTWARE: Pat SOFTWARE: PAT TYPE: PRT TYPE: PRT ORGANISM: Zea US-09-282-305-8 Query Match Best Local Simi Matches 385;	41 86.5 42 86.5 43 86.5 44 86 86	28 88.5 29 88.5 30 88 31 87.5 32 87.5 33 87.5 36 86.5 37 86.5 38 86.5 40 86.5
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LENGTH: 439
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CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Malze Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
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US-08-528-255A-1

Sequence 1, Application US/08528255A Patent No. 5659016 GENERAL INFORMATION:

APPLICANT: NAKAMURA, YUSUKE
APPLICANT: : FURUKAWA, YOICHI
TITLE OF INVENTION: RPDL PROTEIN
TITLE OF INVENTION: ENCODING THE

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE:

THIEL,

BOUTELL & TANIS,

P.C

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GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Baldwin, Steven P.
APPLICANT: Briggs, Steven P.
TITLE OF INVENTION: Maize Histone Deacetylases And
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION UMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
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US-09-282-305-2
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US-09-282-305-2
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LENGTH: 458
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SOFTWARE: PatentIn Ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFP 66
IPSRV-KREAVEPDTKDKDGLK 447
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QRSRLWSGGAYDSDTEDPDSLK 438
                                                                                               LEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVDDDRKP 426
                                                                                                                                                                        GGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQM 366
                                                                                                                                                                                                                                                    LLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLFQCIIKKVMEVYQPDVVVLQCGADSLAGDRLGCFNLSVKGHADCLRFLRSYNVPMMVL
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                                                                                                                                                                                                                                                                                                                                                                                     GAAVKLNRGDADITVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKFHRRVLYVDIDVH 191
                                                                                                                                                                                                                                                                                                                                                                                                         GGSYKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASEADIRRFHSDDYVAFLASATGNPGVLDPRAIKRFNVGEDCPVFDGLFPFCQASAGGSI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSV 126
                                                                           LENIKNMILENLSKIEHVPSTQFHDRPSDPEAPE -- EKEEDMDK---
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63.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 458;
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2026 Rambling Road

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US-08-528-255A-1
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Matches 290; Conserv
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER: 1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: human
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MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
419 DVDDDRKPIPS-----RVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNP 473
                                            366 LFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEFSDSEE
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                                                                                                                                                                                                                                          246
                                                                                                                                                                                                                                                                                  254 GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI 313
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                                                                                                                                                                                                                                                                                                                                                               194 AFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM 253
                                                                                                                                                                                                                                                                                                                                                                                                                               126 KQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVEE 185
                                                                                           374 LLHNLSKLQHAPSVPFQERPPDTETPEV-DEDQEDGDKRWD---
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CITY: Kalamazoo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                            RNVARCRTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQR 365
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                                                                                                                                                                                                                                      SKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGYTI 305
                                                                                                                                                                                                                                                                                                                                    AFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKPVM
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Pred. No. 6.8e-154;
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Patent No. 5763182
                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: lin
MOLECULE TYPE:
ORIGINAL SOURCE:
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NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23-SEP-
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAMURA, YUSUKE APPLICANT: : FURUKAWA, YOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: FURUYA CASE 1335 TELECOMMUNICATION INFORMATION:
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FILING DATE: September 14, 1999
APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER:1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Kalamazoo
STATE: Michigan
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66 KYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLN 125
                                                                                                               14 GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC 73
                                                                                                                                                                        Match 56.2%; Score 1530; DB 1; Local Similarity 59.2%; Pred. No. 6.8e-154;
                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                    74 RFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
                                                                                                                                                                                                                                                                           LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                           6 GTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMT 65
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (616) 381-1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  September 14, 1995
UMBER: JP6-227876
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LENGTH: 432
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                                                                                                                                                                                                                                                                                          Matches 249;
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR EILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
-09-282-305-10
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SOFTWARE: Patentin V
                                                                                         138 DIAINWAGGLHHAKKCEASGECYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFYA 197
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TDRVMTVSFHKYGDLFFPGTGDIKDIGEREGKYYAINIPLKDGIDDTSFTRPFKTIIAKV
                                                                       DIAINWAGGLHHAKKCEASGFCYINDLYLGILELLKYHARVLYIDIDVHHGDGVEEAFYF
                                                                                                                                                                                                                 YFITPIVGDVGNVYFGPNHPMKPHRLCMTHHLVLSYGLHQKMEIYRPHKAYPIELAQFHS 67
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                                                                                                                                            ADYVEFLHRITPDSQHLYASELTRYNLGEDCPVFDNLFEFCQIYAGGTLDAARRLNHKIC 127
                                                                                                                                                                             DDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGLC 137
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                                                                                                                                                                                                                                                                                                         50.0%; Score 1360; DB 4; 59.0%; Pred. No. 6.8e-136;
                                                                                                                                                                                                                                                                                        61; Mismatches 92;
                                                                                                                                                                                                                                                                                                                          Length 432;
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SEQ ID NO 4
LENGTH: 351
TYPE: PRT
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Best Local Similarity
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases
FILE REFERENCE: 5718-44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
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                                                              GGGGYTIRNVARCMCYETAVAVGVEPDNKLPYNDYYEYFGPDYTLHIQPKSVENLNTTKD 264
                                                                                 GGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSROM
                                                                                                                              GLFQCIIKKVMEVYQPDVVVLQCGADSLAGDRLGCFNLSVKGHADCLRFLRSYNVPMMVL
                                                                                                                                                                                                              HGDGVEEAFYATDRWMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYH 246
                                                                                                                                                                                                                                                                                             GGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIH 186
                                                                                                                                                                                                                                                                                                                                                            ARERDLCRYHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSV 126
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                  LEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVDDDRKP 426
                                                                                                                                                                                             HGDGVEEAFFTTNRVMTVSFHKYGDFFPGTGHITDVGAAEGKHYALNVPLSDGIDDTTFR 144
LENIKNMILENLSKIEHVPSTQFHDRPSDPEAPE - - EKEEDMDK - -
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48.9%; Pred. No. 1.2e-111;
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: Sequence 2, Application US/09214564A

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GENERAL INFORMATION:
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Patent No. 6218150
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CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
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APPLICANT: MIYAKE, Kazue
APPLICANT: MUKAI, Hiroyuki
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
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APPLICANT: SATO, Yoshimi
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PRIOR FILING DATE: 1997-11-27
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PRIOR FILING DATE: 1997-06-26
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                                                                                                                                                                                                                                                                                                           254 GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI 313
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                                                                                                                                                                                                                                    RN--VARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIR 371
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                                                                                                                                                                                                                                                                                                                                                                                  FYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYS-LNVPLDDGIDDESYHLLFKPIM 253
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; Pred. No. 2.1e-18;
71; Mismatches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: Sharp, Phillip A.

APPLICANT: Zhou, Qiang

TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional

TITLE OF INVENTION: Elongation By HIV-1 TAT

FILE REFERENCE: M0656/7042

CURRENT APPLICATION NUMBER: US/09/214,564A

CURRENT FILING DATE: 1999-08-18

PRIOR APPLICATION NUMBER: US 60/021,218

PRIOR APPLICATION NUMBER: US 60/033,152

PRIOR FILING DATE: 1996-07-03

PRIOR FILING DATE: 1996-12-13

PRIOR APPLICATION NUMBER: PGT/US97/11713

PRIOR APPLICATION NUMBER: PCT/US97/11713

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 5

COMPRIANDE: ENGINEER 1997-07-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-760-745-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.9%; Score 106; DB 4; Length 754; Best Local Similarity 20.4%; Pred. No. 0.04; Matches 80; Conservative 35; Mismatches 129; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
LENGTH: 754
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08760745 Patent No. 5972658
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                             APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: LUNG GROWTH FACTOR VARIANT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 GVNPVGVE-EASVKMEEEGTNKGGAEQAFPPK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 ---- RGFEGSCSQKESEEGNPVRGSEEDSPKK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 YSLNVPLDDGIDDESYHLLFKPIMGKVMEIFRPGAV-----VLQCGADSLSGDRLGCF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 YVSGLPPDITVDE-----FIQLMSKFGIIMRDPQTEEFKVKLYKDNQGNLKGDGLCCYL 189
                                                                                        STREET: 3174 PO:
CITY: Palo Alto
STATE: CA
                                 COUNTRY: U
ZIP: 94304
                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NLSI-----KGHAECVKFMRSFNVPLLLLGGGGYTIRNVARCWCYETGV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGMAFEEPIDEKKFEKTEDG--GEFEEGASENNAKESSPEKEAEEGCPEKESEEGCPK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFGQIRKLLLFDRHPDGVASVSFRDPEEADYCIQTLDGRWFGGRQITAQAWDGTTDYQVE\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMQQKQLDWRPERR----AGPSRMRHERVVIIKNMFHPMDFEDDPLVLNEIREDLRVECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALGVEVEDKMPEHEYYEYFGPDYTLH---VAPSN----MENKNSRQMLEEIRNDLLHNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRESVELALKLLDEDEIRGYKLHVEVAKFQ------LKGEYDASKKKKKCKDYKKKL
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                                                                SD
                                                                                                                                                                              INCYTE PHARMACEUTICALS,
                                                                                                                                                  Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129; Indels 148;
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MEDIUM TYPE;

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                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08568459A Patent No. 5849306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 48;
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                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEORMATION FOR SEQ ID NO:
                                                                                                                                         APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Weilems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    APPLICANT: Chitnis, Chetan APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                             APPLICANT:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: USIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 TGVNPVGVEEASVKMEEEGTNK 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 NDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMD-----VDDDRK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 DKMPE-----HEYYE-YFGPDYTLHVAPSNM------ENKNSRQMLEEIR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 EKNEKGALKRRAGDLLEDSPKRPK-EAENPEGEEKEAATLEVERPLPMEVEKNSTPSEPG 205
            CITY: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 3.9%; Score 105; DB 2; Length 240; Local Similarity 23.8%; Pred. No. 0.0075; res 48; Conservative 27; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US
FILING DATE: Herewith
                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 NNPTVKASGYQSSQKKSCVEEP----EPEPEAAEGDGDKKGNAEGSSDEEGKLVIDEPAK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 DEMPEAAVKSTANKYQVFFFGTHETAFLGPKDLFPYEESKEKFGKPNKRKGFSEGLWEIE 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGRGPPQEEEEEEDEEEEATKE 227
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92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                             E: Knobbe Martens Olson & Bear 620 Newport Center Drive 16th
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                                                                                                                                                                                                                                                                                                             Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank
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                                                                                 16th Floor
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Best Local Similarity
Thehes 76; Conserve
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REFERENCE/DOCKET NUMBER: NIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                             sequence 4, Application US/08487826B
Patent No. 5993827
                                                                                                                           GENERAL INFORMATION:
                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: pr
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                     APPLICANT:
                                                           APPLICANT:
APPLICANT:
                 APPLICANT:
                                                                                                                                                                                                                                                                           835 IGSSPNDNINVTEQGD-NISGVNSKPLSDDVRPDKKELEDQNSDESEE 881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 NVARCWCYETGVALGVEVEDKMPEHEYYEY-FGPDYTLH-----VAPSNMENKNSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 GDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGY-----TIR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 LLMIKEH----ILAIAIYESRILKRKYKNKDDKEVCKIINKTFADIRDIIGGTDYWNDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 LELLKQHERVLYVDIDIHHGDGVEEAFYATD-----RVMTVSFHKFGDYFPGTGHIQDIG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                               721 LNFEDEFKEELHSDYKNKCTMCPEVKDVPISIIRNNEQTSQEAVPEENTEIAHRTETPSI 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino aci
STRANDEDNESS: s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                               SEGPK-GNEQKERD-----DDSLSKISVSPENSRPETDAKDTSNLLKLKGDVDISMPKAV
                                                                                                                                                                                                                                                                                                                                                                                                     DEDQEDGDKRWDPDSDMDVDDDRKPIPSRVKREAVEPDTKDKDGL------KGI 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKSKCNSYKEWISKKKEEYNKQAK-QYQEYQKGNNYKMYSEFKSIKPEVYLKKYSEKCSN 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRKLVGKINTNSKYVHRNKKNDKLFRDEWWKVIKKDVWNVISWVFKDKTV---CKEUDIE 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YGSGKYYSLNVPLDDGIDDESYHLLFKPINGKVMEIFRPGAVVLQCGADSLS 275
                                                                                                                                                                                                                                                                                                                   MERGKGCEVEVDESGSTKVTGVN--PVGVEEASVKMEEEGTNKGGAEQ 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QMLEEIRNDLLHNLSKLQHAPSVPF------QERPPD-----TETPEV 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1435 amino acids
                                                           Chitnis, Chetan
Miller, Louis H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                       Peterson, David S.
                                                                                                     Sim, Kim L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                 Xin-zhaun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5%; Score 96; DB 2; Length 1435;
18.6%; Pred. No. 1.4;
vative 61; Mismatches 155; Indels 116;
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Best Local Similarity 18.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 235-017 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ISTAELSEN, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 LLMIKEH----ILAIAIYESRILKRKYKNKDDKEVCKIINKTFADIRDIIGGTDYWNDLS 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 LELLKQHERVLYVDIDIHHGDGVEEAFYATD-----RVMTVSFHKFGDYFPGTGHIQDIG 223
  835
                                       450 MERGKGCEVEVDESGSTKVTGVN--PVGVEEASVKMEEEGTNKGGAEQ 495
                                                                                                                                                                 721 LNFEDEFKEELHSDYKNKCTMCPEVKDVPISIIRNNEQTSQEAVPEENTEIAHRTETPSI 780
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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IGSSPNDNINVTEQGD-NISGVNSKPLSDDVRPDKKELEDQNSDESEE 881
                                                                                                                          DEDQEDGDKRWDPDSDMDVDDDRKPIPSRVKREAVEPDTKDKDGL-----KGI 449
                                                                                                                                                                                                                                                                                                                                                                               GDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGY-----TIR------
                                                                                SEGPK-GNEQKERD----
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                                                                                                                                                                                                         -QMLEEIRNDLLHNLSKLQHAPSVPF------QERPPD-----TETPEV 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1435 amino acids
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PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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                                                                                -DDSLSKISVSPENSRPETDAKDTSNLLKLKGDVDISMPKAV 834
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Pred. No. 1.4;
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: NAME/KEY: Domain
: LOCATION: 657..723
: OTHER INFORMATION:
US-07-814-964-11
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APPLICANT: Donahu
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
PILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION LANDORMATION:
TELEPHONE: 617-861-6240
TELEPAX: 617-861-9540
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy disk
                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                      FEATURE:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                      NAME/KEY: Domain LOCATION: 518..547 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                           NAME/KEY: Domain LOCATION: 632..649 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: U. FILING DATE: 19911226
                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                     NAME/KEY: Domain
LOCATION: 458..507
                                                                                                                                                                                                                                                                                                                                       CLONE:
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02173
                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                            LOCATION:
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Toney, Jeffrey |
Bruhn, Suzanne
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547..620
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                                                                                                                                                                                                                                                                               ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569 T---RESIKRENPGIKVTEIAKKGG 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 FEEISSVNFARS------GGST-----RSFDFEVTLKNGTVHIFSSIEKEEYAKLF 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 SLDPPIKQG--QTRYHYLVLLFAPDEETTIELPFSEAELRDKYEGKLEKEISGPVYEVMG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 SLNVPLDDGIDDESYH---LLFKP-----IMG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 KVMEIF-----RPGAVVLQCGADSLSGDRLGCFNLSIKGH-----
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
REGISTRATION NUMBER:
                                                                                                                                FILING DATE: CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive CITY: Lexington
                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RKP1PSRVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTK-----VTGVNP 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --DYITQKKLHV--SNMGKDKSGYKDVDFGDSD-------NENEPDAYLAR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPDY----TLHVAPSNM-ENKNSRQMLEEIRNDLLHNLSKLQHAPSVPFQERPPD----- 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGAKKKKEKKSEKKEKKEKKHKEK-----ERTKKPSKKKKDSGKPKRATTAFMLWLND 566
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                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kellett, Patti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown, Steven
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Bruhn, Suzanne L.
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                                                                                                                                                                               US/08/258,442
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MTTELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-9540
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569 T---RESIKRENPGIKVTEIAKKGG 590
                                   474 VGVEEASVKMEEEG----TNKGG 492
                                                                                                                                                                                                                                                                                      371 FEEISSVNFARS------GGST-----RSFDFEVTLKNGTVHIFSSIEKEEYAKLF 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 SLNVPLDDGIDDESYH---LLFKP------IMG 254
                                                                                                                                                                                                                                                                                                                                                                                              255 KVMEIF------RPGAVVLQCGADSLSGDRLGCFNLSIKGH-----
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LOCATION: 632..64
OTHER INFORMATION:
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                                                                                                                                           LKAEAREKEEDDDDGDSDEESTDEDFKPNENESDVAEEYDSNVESDSDDDSDASGGGGDS 515
                                                                                                                                                                                                                 -- DY ITQKKLHV -- SNMGKDKSGYKDVDFGDSD ---
                                                                                                                                                                                                                                                 GPDY----TLHVAPSNM-ENKNSROMLEEIRNDLLHNLSKLQHAPSVPFQERPPD-----
                                                                                                                                                                                                                                                                                                                                                           KVMKVLIGRKITGPGNFIGHSGTAA-----VGCSFKAAAGYLYPLERGFIYIHKPPLHIR 370
                                                                      DGAKKKKEKKSEKKEKKEKKHKEK-----
                                                                                                      ----RKPIPSRVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTK-----VTGVNP 473
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518..547
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547..6
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                                                                      -ERTKKPSKKKKDSGKPKRATTAFMLWLNU 568
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US-08-328-809-6

Sequence 6, Application US/08328809 Patent No. 5705334

Patent No. 5705334 GENERAL INFORMATION:

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LOCATION: 657..723

COTHER INFORMATION: //
US-08-328-809-6
Query Match 3.5%;
Best Local Similarity 20.8%;
Matches 80; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,809
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: FENION, GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kellett, Patti
TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                   NAME/KEY: Domain LOCATION: 547..620 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                   NAME/KEY: Domain LOCATION: 518..547 OTHER INFORMATION:
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TYPE: amino acid
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ZIP: 02109
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
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LOCATION: 458..507
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Toney, Jeffrey H.
Bruhn, Suzanne L.
Pil, Pieter M.
                                                                                                                                                                                    Domain
632.,649
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; Score 94.5; DB 1;
; Pred. No. 0.63;
38; Mismatches 92;
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 92;
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T---RESIKRENPGIKVTEIAKKGG
                              VGVEEASVKMEEEG----TNKGG 492
                                                                                                                                                                                                     GPDY----TLHVAPSNM-ENKNSRQMLEEIRNDLLHNLSKLQHAPSVPFQERPPD-----
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                                                                                                                                                                                                                                                                                                                                                                     SLDPPIKQG--QTRYHYLVLLFAPDEETTIELPFSEAELRDKYEGKLEKEISGPVYEVMG
                                                                                                                      LKAEAREKEEDDDDGDSDEESTDEDFKPNENESDYAEEYDSNVESDSDDDSDASGGGGDS
                                                                                                                                                                                                                                                                                                       KVMKVLIGRKITGPGNFIGHSGTAA-----VGCSFKAAAGYLYPLERGFIYIHKPPLHIR
                                                                                                                                                                                                                                                                                                                                   KVMEIF-----RPGAVVLQCGADSLSGDRLGCFNLSIKGH-
                                                            DGAKKKKEKKSEKKEKKEKKHKEK - - - - - -
                                                                                        ----RKPIPSRVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTK-----VTGVNP
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                                                                                                                                                      --TETPEVDEDQEDGD---
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 590
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Search completed: April 26, 2002, 17:51:24 Job time: 32 sec

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Result
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Perfect score:
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A_Geneseq_1101:*
1: /SIDSB/gcgdata/
2: /SIDSB/gcgdata
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5: /SIDSB/gcgda'
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10: /SIDSB/gcg'
11: /SIDSB/gcg'
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A partial deacetyl	AAW29330	18	125	5.	456	36
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e histone	AAY28801	20	432	0	1360	23
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## ALIGNMENTS

RESULT AAB67811

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Protein; 501 AA

Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase CA2316036-A1. Histone deacetylase; AtRPD3A; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation. N-PSDB; Miki B, Arabidopsis thaliana Amino acid sequence of a histone deacetylase designated AtRPD3A. 29-JUN-2001 (first entry) AAB67811; (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA 24-AUG-2000; 2000CA-2316036. 27-FEB-2001. 2001-258457/27. DB; AAF80350. Brown D, 99US-0383971. Tian Ļ 2 ~

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suppressing expression of selected gene for treating cancer, involves introducing peptide comprising nucleic acid binding portion that binds to or associated with selected gene and chromatin inactivation portion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2722; DB 22; pred. No. 3.7e-275; ); Mismatches 0;
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                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                             rice, soybean and wheat nucleic acid fragments encoding HD1. It also relates to the construction of a chimeric gene encoding all a portion of HD1, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HD1 in a transformed host cell. The availability of
                                                                                                                                                                                                                                                                                                                                nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in eukaryotic ceils, and will also provide mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HD1), a chromatin associated protein, as deduced from a soybean root cDNA clone (see AAZ58260) isolated on the basis of homology plant histone deacetylases. The invention relates to isolated
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                     control transcriptional gene regulation in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of soybean histone deacetylase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 27-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transforming plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid fragment useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DUPO ) DU PONT DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          soybean; transgenic plant; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chromatin associated protein; histone deacetylase gene 1; HD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean histone deacetylase 1 (HD1) protein
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   181
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                                                                                                                                                                  1 MDTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQ 60
                                                                                                        VLKPFPARERDICRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQT 120
VDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGI 24(
                                            YAGGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLY 180
                                                                                        vlkpmaakdrdlckfhaddyvaflrgitpetqqdqlrqlkrfnvgedcpvfdglysfcqt 120
                                                                                                                                                 mesggnslpsgsdgvkrkvsyfydpevgnyyyggghpmkphrirmthallahygllqhmq 60
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                            yaggsvggalklnhgvcdiainwagglhhakkceasgfcyvndivlailellkihervly
                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                          473 AA;
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80.7%;
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                                                                                                                                                                                                             33;
                                                                                                                                                                                                             Score 2138; DB 21;
Pred. No. 3.5e-214;
3; Mismatches 37;
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The present sequence is maize histone deacetylase encoded by HD cDNA belonging to family 1, ZmHD1. This enzyme responsible for removing acetyl modifications, may be localised to promoters targeted for repression by other proteins that associate with HD and specifically bind regulatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transgenic plants with increased disease resistance. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize histone deacetylase; HD; HD cDNA; family 1, ZmHD1; gene repression: acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 63-65; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease response promoter
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                                                          by histone deacetylase
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Sequence

transforming plants

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Best Local Sim
Matches 385;
              New nucleic acid fragment useful as probes and
                                      N-PSDB; AAZ58259
                                                                                                   (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                       13-JUL-1999;
                                                                                                                                                                              27-JAN-2000
                                                                                                                                                                                                         WO200004177-A1
                                                                                                                                                                                                                                                                    Chromatin associated protein; histone deacetylase gene 1; HD1;
                                                                                                                                                                                                                                                                                          Rice histone deacetylase 1 (HD1) protein (C-terminal portion)
                                                                                                                                                                                                                                                                                                                      08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                      AAY58828 standard; Protein;
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                                                    2000-182439/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sggnslpsvgpdgqkrrvcyfydpdvgnyyygqghpmkphrirmthsllarygllnqmqv 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant; transcription regulation
                                                                            RΕ,
                                                                            Vollmer
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RESULT AAY28799 ID AAY2

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AAY28799 standard; protein; 439

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Maize histone

deacetylase-3

13-JAN-2000 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a C-terminal portion of rice CC histone deacetylase 1 (HD1), a chromatin associated protein, as CC deduced from a cDNA contig (see AaZ58259) obtained from cDNA clones CC isolated from rice callus, 15-day-old leaf and 15-day-old seedling CC construction on the basis of homology to other plant histone CC deacetylases. The invention relates to isolated rice, soybean and CC wheat nucleic acid fragments encoding HD1. It also relates to the CC construction of a chimeric gene encoding all or a portion of HD1, CC in sense or antisense orientation, where expression of the chimeric CC gene results in production of altered levels of HD1 in a transformed host cell. The availability of nucleic acid sequences CC encoding (portions) of histone deacetylase proteins will facilitate Studies of global transcriptional regulation in eukaryotic cells, CC and will also provide mechanisms to control transcriptional gene
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                                                             LQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVDDDRKPIPS-----R 430
                                                                                                                                                                                                                                       CYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEE1RNDLLHNLSK 380
                                                                                                                                                                                                                                                                                      RPGAVVLQCGADSLSGDRLGCENLSIKGHAECVKFMRSFNVPLLLLGGGGYTIRNVARCW 320
                                                                                                                                                                                                                                                                                                                                                         VMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGKVMEIF
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                                                                                                  VKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTK---VTGVNPVGVEE-ASVKMEEE 486
                                                                                                                                                                                                   cyetgvalgheltdkmppneyfeyfgpdytlhvapsnmenkntrqqlddirsrlldnlsk 359
                                                                                                                                                                                                                                                                                                                                                                                                         INWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFYATDR 200
                                                                                                                                  lrhapsvqfqerppeaelpeqdedqedpderhhadsdvem-ddvkplddsgrrssiqnvr 418
                                                                                                                                                                                                                                                                        rpgavvlqcgadslsgdrlgcfnlsirghaecvrfmrsfnvpllllggggytirnvarcw
                                                                                                                                                                                                                                                                                                                                        vmtvsfhkfgdyfpgtgdirdighskgkyyslnvplddgiddesygslfkpimgkvmevf
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78.1%;
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Pred. No. 2.9e-200;
6; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize histone deacetylase; HD; HD cDNA; family 1, ZmHD1; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity; disease response promoter.
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N-PSDB; AAX90839.
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                                                                                            GGNSL-ASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVL 62
                                                                                                                                                                                                                                                                                        LLLLGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKN
                                                                                                                                                        IDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDD
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                                                                                                                                                                                                                                                      KPFPARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYA 122
trhqlddiksklldnlsklrhapsvqfqerppeaelpeqdedkenpderhdadsdvem-n
                                                                                                                                            idihhgdgveeafyttdrvmtvsfhkfgdyfpgtgdirdvghskgkyyslnvplddgidd
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58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease resistance
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84.2%;
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Pred. No. 1.2e-194;
29; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           termination sequence.
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14-JUL-1999; 99US-0144 16-JUL-1999; 99US-0144 16-JUL-1999; 99US-0144 19-JUL-1999; 99US-0144 19-JUL-1999; 99US-0144 19-JUL-1999; 99US-0144 19-JUL-1999; 99US-0144 19-JUL-1999; 99US-0144 20-JUL-1999; 99US-0144 20-JUL-1999; 99US-0144 21-JUL-1999; 99US-0144 21-JUL-1999; 99US-0144 21-JUL-1999; 99US-0144 21-JUL-1999; 99US-0144 21-JUL-1999; 99US-0144 21-JUL-1999; 99US-0144 22-JUL-1999; 99US-014	PR 18-JUN-1999 99US-0133 PR 18-JUN-1999 99US-0134 PR 18-JUN-1999 99US-0134 PR 18-JUN-1999 99US-0135 PR 18-JUN-1999 99US-0135 PR 18-JUN-1999 99US-0135 PR 18-JUN-1999 99US-0136 PR 18-JUN-1999 99US-0136 PR 18-JUN-1999 99US-0136 PR 18-JUN-1999 99US-0136 PR 23-JUN-1999 99US-0144 PR 23-JUN-1999 99US-0144 PR 23-JUN-1999 99US-0144 PR 30-JUN-1999 99US-0144 PR 30-JUL-1999 99US-0144 PR 01-JUL-1999 99US-0144	PR 07-MAY-1999; 99US-0132863. PR 11-MAY-1999; 99US-0134256. PR 14-MAY-1999; 99US-0134219. PR 14-MAY-1999; 99US-0134221. PR 14-MAY-1999; 99US-0134221. PR 18-MAY-1999; 99US-013476. PR 19-MAY-1999; 99US-0135124. PR 21-MAY-1999; 99US-0135124. PR 21-MAY-1999; 99US-0135021. PR 25-MAY-1999; 99US-0136021. PR 27-MAY-1999; 99US-0136021. PR 27-MAY-1999; 99US-0136021. PR 03-JUN-1999; 99US-0137522. PR 03-JUN-1999; 99US-0137522. PR 03-JUN-1999; 99US-0137522. PR 04-JUN-1999; 99US-0138094. PR 10-JUN-1999; 99US-0138419. PR 16-JUN-1999; 99US-0138427. PR 16-JUN-1999; 99US-0139455. PR 18-JUN-1999; 99US-0139455.

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                            Arabidopsis thaliana
                                            Histone deacetylase; AtRPD3B; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation.
                                                                                                     AAB67812;
                                                                    Amino acid
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293; Conserv
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nilarity 60.9%;
Conservative 64
                                                                   sequence of a histone deacetylase designated AtRPD3B
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Pred. No. 1.1e
54; Mismatches
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1.1e-154;
hes 93; In
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designated ARRPD3B. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant, particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYAGGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQV 61
                                   tatyesdsddddkp-
                                                              --DSDMDVDDDRKPIPSRVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVN
                                                                                                                                                                                                                       \verb|nvplmvlggegytirnvarcwcyetavavgvepdnklpyneyfeyfgpdytlhvdpspme|
                                                                                                                                                                                                                                                                                                                       mddesfrslfrpliqkvmevyqpeavvlqcgadslsgdrlgcfnlsvkghadclrflrsy
                                                                                                                                                                                                                                                                                                                                                                    IDDESYHLLEKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YVDIDIHHGDGYEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             desgislpsgpdgrkrrvsyfyeptigdyyyggghpmkphrirmahsliihyhlhrrlei 63
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DB; AAF80351.
                                                                                                                                                                             NKNSRQMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDP----
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Pred. No. 7.5e
64; Mismatches
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hes 94;
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AAY28797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize histone deacetylase; HD; HD cDNA; family 1, ZmHD1; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-611038/52
N-PSDB; AAX90837.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New deacetylase genes, used for producing transgenic plants which have increased disease resistance -
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HGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYH
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                                                                        GGSYKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIH 186
                                                                                                                                                                                                                  ARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSV 126
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Pred. No. 1.4e-152;
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Indels Length 458;

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Gaps

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AAW29324

AC AAW294

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                                                                                           influencing cell cycle progression or to modulate gene transcription. The products can be used for diagnosis and therapy. They can be used, for example, to treat tumours or proliferative disorders or spermatogenesis, osteogenesis, chondrogenesis or the differentiation of progenitor cells. They can also be used to treat psoriasis, bone diseases, fibroproliferative disorders, degenerative disorders, or for repair of cartilage, increasing bone density, liver repair subsequent to a partial hepatectomy, to promote regeneration of lung tissue in the treatment of emphysema, or for inducing tolerance in autoimmune diseases, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated histone deacetylase polypeptide(s) and genes -develop products for modulating the proliferation, survival differentiation of cells, e.g. for treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Histone deacetylase gene: HDx; HDl; HDx polypeptide; H4; cell differentiation; chromatin structure; cell opposition of the proliferative disorder; fibroproliferative disorder;
                                   transplant recipients. HDx inhibitors can be used as anti-fungal a preservatives in foodstuff, feed supplements for promoting weight
                                                                                                                                                                                                                                                                                                                                                                                                                proteins are able to alter chromatin structure by deacetylating histones such as H3 or H4. They have the ability to modulate cell growth by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide, designated HD1. The HDx polypeptides are capable of modulating proliferation survival and differentiation of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a novel histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Pages 112-114; 159pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         degenerative disorder; autoimmune disease; HDx inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel histone deacetylase (HDx) protein, designated HD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also be used in cell cultures.
note: in the claims, the full length HD1 sequence is incorrectly referred to as SEQ. ID. No.2; from the disclosure it is clear that HD1
                                                                                                                                                          Human; gene expression;
chromatin inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                  W0200102019-A2
                                                                                                                                                                                                     Human
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                                                                                                                                                       disease model; treatment; suppression; DNA binding site; histone deacetylation
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method of suppressing the expression a gene of interest by introducing into the cell a protein containing a DNA binding site and a chromatin inactivation portion, or a nucleotide encoding such a peptide. Preferably the chromatin inactivation portion part of the histone deacetylation (HDAC) complex. The method can be use in disease treatment, for example in the treatment of cancer by the suppression of oncogenes, and in the production of disease models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suppressing
                   08-MAR-2001
                                                                                 AAB49954 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 65pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         essing expression of selected gene for treating cancer, involves ducing peptide comprising nucleic acid binding portion that binds associated with selected gene and chromatin inactivation portion
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                  (first entry)
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-6 and HDAC-D. These inhibitors may be antisense strands or they may be compounds identified by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and for identifying which histone deacetylase is involved in a neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms neoplasia, or for inhibiting neoplastic cell growth in an animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human histone deacetylase HDAC-1.
                419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                       DYDDDRKPIPS-----RVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNP
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                                                                             LLHNLSKLQHAPSVPFQERPPDTETPEV-DEDQEDGDKRWD--
                                                                                                                            RNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRND
                                                                                                                                                                                                        GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI
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                                                                                                                                                                                                                                                                                                   kqqtdlavnwagglhhakkseasgfcyvndivlailellkyhqrvlyididihhgdgvee
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                                            lten1rm1phapgvqmqaipedaipeesgdededdpdkrisicssdkriaceeefsdsee
                                                                                                         {\tt rnvarcwtyetavaldteipnelpyndyfeyfgpdfklhispsnmtnqntneylekikqr}
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59.4%;
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                                                                        Matches
                                                                                        Query Match
Best Local :
                                                                                                                                                                                                           gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present AAB57303 represent sequences.
                                                                                                                                                                                                                                                             and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                    cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                     proteins, called prostate cancer antigens, given in AAB56363 to AAB57302 The prostate cancer antigens can have neuroprotective, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                       AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 2005-2006; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate cancer associated gene sequences, referred to cancer antigens, useful for treatment, prevention, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAF16188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate cancer antigen protein sequence SEQ
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   12
                                    14 GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC 73
                                                                                        Local Similarity
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egeggrknssnfkkakrvkte----dekekd-----peekk----evteeektkeekpea 472
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                                                                    Score 1544; DB 21;
Pred. No. 4.2e-152;
7; Mismatches 98;
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RESULT 1
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  AAR88919 is a transcriptional control protein, RPI human foetal lung cDNA library. The gene encoding
                                        Claim 1; Page 10-12; 15pp; English.
                                                                                 New human transcriptional control protein RPDL - used to develop prods. for study and diagnosis involving the protein, partic. for
                                                                                                                                                                                                                                                                                                                                                                              Transcription; expression; control; diagnosis; study; cancer; mammary; gastric carcinoma; chromosome 1p34.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR88919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR88919 standard;
                                                                                                                            N-PSDB; AAT12940
                                                                                                                                                                                             (CANC-) CANCER INST. (EISA) EISAI CO LTD.
                                                                                                                                                                                                                                         22-SEP-1994;
                                                                                                                                                                                                                                                                   21-SEP-1995;
                                                                                                                                                                                                                                                                                                24-APR-1996
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                   Furukawa Y, Nakamura
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                                                                                                                                                                                                                                                                                                                                                                                                                        foetal lung-derived transcriptional control protein.
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at 1p34.1 on the short arm of chromosome 1, this is a region where a deletion is recognised in mammary and gastric carcinomas. The RPDL gene is an important gene and has been found to be expressed in all the following human tissues: heart, kidney, liver, lung, pancreas, placenta, skeletal muscle, large intestine, peripheral leukocyte, ovary, prostate, small intestine, spleen, testis and thymus gland; but is not present in brain tissue. RPDL cDNA exhibits homology with the yeast transcription factor RPD3 and is believed to have a similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function. RPDL and DNA encoding it can be used in studying the interactions of the protein with DNA and other proteins in the cell.
473 kgvke-evkl 481
                                     474 VGVEEASVKM 483
                                                                            426
                                                                                                            419 DVDDDRKPIPS-----RVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNP 473
                                                                                                                                                                                       374 LLHNLSKLQHAPSVPFQERPPDTETPEV-DEDQEDGDKRWD---
                                                                                                                                                                                                                           306 rnvarcrtyetavaldteipnelpyndyfeyfgpdfklhispsnmtngntneylekikgr 365
                                                                                                                                                                                                                                              314 RNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSROMLEEIRND 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 lfen1rm1phapgvqmqaipedaipeesgdededdpdkrisicssdkriaceeefsdsee 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC 73
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                                                                         egeggrknssnfkkakrvkte----dekekd-----peekk----evteeektkeekpea 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.2%; Score 1530; DB 17; 59.2%; Pred. No. 1.2e-150; tive 67; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Search completed: April 26, 2002, 17:52:13 Job time: 81 sec

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
         SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_humao:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_orqane1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_vertebr
13: sp_vertebr
14: sp_unclass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                473505 seqs, 146272329 residues
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Gapop 10.0 , Gapext 0.5
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2544
1 MEADESGISLPSGPDGRKRR.....TGEDEMDDDNPEPDVNPPSS 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
sp_fungi:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match Length		<b>B</b> 0	ID	Description
1	2542	6.66	471	10	Q9FVE5	Q9fve5 arabidopsis
2	2535	99.6	471	10	Q9FML2	
w	1738	68.3	458	10	Q9ZTP8	
4	1560.5	61.3	501	10	Q9SZL3	arabidops
ري د	1522	59.8	500	10	Q9LKG1	_
6	1496.5	58.8	493	10	Q9AXF0	U
7	1476	58.0	521	ري.	077213	077213 drosophila
8	1476	58.0	521	σı	Q9VZA1	Q9vzal drosophila
9	1373	54.0	687	ىپ	Q9P4F5	Q9p4f5 emericella
10	1369	53.8	409	10	Q9FH09	Q9fh09 arabidopsis
11	1305.5	51.3	465	ហ	062339	062339 caenorhabdi
12	1292.5	50.8	428	11	Q99PA0	Q99pa0 rattus norv
13	1288	50.6	444	ഗ	Q9GUA8	Q9qua8 cryptospori
14	1284	50.5	648	w	Q9C1C6	
15	1281	50.4	449	ഗ	Q9XYC7	Q9xyc7 plasmodium
16	1277.5	50.2	428	11	80ML60	Q9jm08 mus musculu
17	1275.5	50.1	428	11	Q9JLX5	Q9jlx5 mus musculu
18	1275	50.1	405	w	059702	059702 schizosacch
19	1233.5	48.5	438	υī	Q9VNC2	Q9vnc2 drosophila

45 265	44 266.5	43 268															28 748.5								
10.4	10.5				10		11							18	23	23	29.4	31	32	32	39	42	45		
878	577	338	796	425	1114	1108	883	158	310	380	389	389	367	375	223	256	428	377	377	377	481	429	437	419	566
4	10	_	υ,	10	11	10	σ	10	N	2	N	N	N	2	4	11	σ	4	4	11	w	υ	J	10	w
Q9UFU7	Q9LS38	Q9HSP7	017323	Q9SJE6	Q9JL73	Q9FNQ7	Q9XYX1	Q9LXN8	067877	Q9н <b>хм1</b>	Q99TC9	Q9K7X1	Q9WX04	067135	Q9н368	Q99PA2	Q9GRP1	Q9NYH4	Q9NP76	Q9D0 <b>K</b> 6	Q9P4F4	Q9GT74	Q9GU59	Q9M1N6	Q9HDT2
Q9ufu7 homo sapien	Q91s38 arabidopsis	Q9hsp7 halobacteri	017323 caenorhabdi	Q9sje6 arabidopsis	Q9j173 mus musculu	Q9fnq7 arabidopsis	Q9xyx1 drosophila	Q91xn8 arabidopsis	067877 aquifex aeo		Q99tc9 staphylococ		Q9wx04 streptomyce	067135 aquifex aeo	Q9h368 homo sapien	Q99pa2 rattus norv	Q9grp1 leishmania	09nyh4 homo sapien	Q9np76 homo sapien	Q9d0k6 mus musculu	09p4f4 emericella	Q9gt74 tetrahymena	Q9gu59 cryptospori	Q9mln6 arabidopsis	09hdt2 ustilago ma

## ALIGNMENTS

01 LEISKESLAUASDIGKEHSPEIVDELASVSPESMGDESAARNIKKENVGEDGPVEDGLED 120 121 FCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGECYVNDIVLGILELLKMEK 180	Qy Oy	
61 LEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFD	3 8	
I MEAUESGISLESGPUGKKKVSYFYEPTIGDYYYGGGFPMKPHKLRMAHSLIIHYHLHRR 	B 2	
C D	Que Bes Mat	
SEQUENCE 471 AA; 52720 MW; 371BF7040E508849 CRC64;	SQ	
Pfam; PF00850; Hist_deacetyl; 1. PRINTS: PR01270: HDASUPER	DR DR	
EMBL; AF195548; AAG28475.1; InterPro; IPR000286; His_deacetylse.	DR DR	
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.	R.	
"Functional analysis of RPD3 histone deacetylase homologs in	3 23	
Wu K., Malik K., Tian L., Brown D., Miki B.;	RA	
STRAIN=CV. COLUMBIA;	R R	
CECUTENCE EDOM N >	R	
[_Tax	OX	
eurosids II; Brassicales; Brassicaceae; Arabidopsis.	8	
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	8	
Eukarvota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:	8	
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IVE HIS	DE	
(TrEMBLrel. 17,	PΤ	
(TrEMBLrel. 16,	ŊΪ	
01-MAR-2001 (TremBirel, 16, Created)	Ŋ	
Q9FVE5 PRELIMINARY; PRT; 471 AA.	AC ID	
Ü	Q9FVE5	
<u>13</u>	RESULT	

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                                                                                                                                                                                                                      Query Match
Best Local S
Matches 469
                                                                                                                                                                                                                                                                                                Sequence features of the regions of 1, physically assigned P1 clones."; DNA Res. 4:401-414(1997).
EMBL; AB008265; BAB10553.1;
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheon
Spermatophyta; Magnollophyta; eudlcotyledons; core eudlcots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HISTONE DEACETYLASE.
                                                                                                                                                                                                                                                                                                                                                                                     "Structural analysis of Arabidopsis thaliana c
Sequence features of the regions of 1,191,918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9FML2;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FML2
                                                                                                                                                                                                                                                                                                                                                                                                                   Tabata S.;
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 181
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                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTATYESDSDDDDKPLHGYSCRGGATTDRDSTGEDEMDDDNPEPDVNPPSS
            RVLY1DIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPL
                                                                   FCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFK
                                                                                                                                                                              MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPL
RVLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPL\\
                                                                                                                         LEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFD
                                                                                                                                                                MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRR
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                                                      FCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFK
                                                                                                           LEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFD
                                                                                                                                                                                                                                                                                                                                                                                                                          Υ.,
                                                                                                                                                                                                                                                                                           471 AA;
                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sato
                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9501997;
S., Kaneko T.,
                                                                                                                                                                                                                                 99.6%;
                                                                                                                                                                                                                                                                                           52651 MW;
                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                   Score 2535; DB 10;
Pred. No. 1.9e-197;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                         CA16C2640D1B1732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                              Asamizu
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Best L
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Q9ZTP8;
Q1-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. CUZCO;

Pipal A., Wegener S.;

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ

EMBL; AF045473; AAD10139.1; -.

Mendel; 39025; Zeama; 3043; 39025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; Elliopsida; Poales; Poaceae; PACC of Panicodeae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HISTONE
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HD1B
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                       297
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                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                1 MEADESGISLPS---GPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHL
                                                                  GTATYESDSDDDDKPLHGYSCRGGATTDRDSTGEDEMDDDNPEPDVNPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVDPSPMENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRP-
                       CLRFLRSYNVPMMVLGGGGYTIRNVARCWCYETAVAVGVEPDNKLPYNDYYEYFGPDYTL
                                 CLRFLRSYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTL
                                                                                                                                                            DGLFPFCQASAGGSIGAAVKLNRGDADITVNWAGGLHHAKKSEASGFCYVNDIVLAILEL
                                                                                                                                                                                  DGLFDFCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILEL 175
                                                                                                                                                                                                         HRLLELSRPYPASEADIRREHSDDYVAFLASAT----GNPGVLDPRAIKRENVGEDCPVF 116
                                                                                                                                                                                                                      HRRLEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSA--ARNLRRFNVGEDCPVF 115
                                                                                                                                                                                                                                                      MAASGEGVSLPSPAGGEDAHRRRVSYFYEPSIGDYYYGQGHPMKPHRIRMAHSLVVHYGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFL
                                                                                                                                                                                                                                                                                                 328;
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                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999 (TrEMBLrel.
2001 (TrEMBLrel.
DEACETYLASE.
                                                                                                                                                                                                                                                                                                                                                          458 AA;
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(TrEMBLrel. 10,
(TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                  Conservative
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Last sequ
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Pred. No. 8.5e-133;
Pred. No. 8.5e-133;
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Last annotation update)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR 2000) to the EMBL/GenBe
EMBL; AL03558; CAB37553.1;
EMBL; AL16159; CAB80478.1;
Interpro; IPR000286; His_deacetylse.
Pfam; PF00850; His_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HISTONE DEACETYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bevan M.,
Mayer K.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SZL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9SZL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wedler H., Kutzner M., Wambutt R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                               YIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDG
                                                                                                                                                                                                                                                                                                                                                                                            DESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEI
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                                                                                                                                                                                                                                                                                                               SRPSLADASDIGRFHSPEYYDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCR 123
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                                                                                                                                                                                                        TYAGGSYGGSYKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVL
                                                                                                                                                                                                                                                                                          LKPFPARDRDLCRFHADDYVSFLRSITPETOOD--QIRQLKRFNVGEDCPVFDGLYSFCQ
                                                                                                                                                                                                                                                                                                                                                                       DTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQV
                                                                                                                         YVDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDG
                                        {\tt IDDESYHLLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wedler H., Kutzner M., X., Schueller C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.3%; Score 1560.5; DB 10; Length 501; 60.7%; Pred. No. 2.4e-118; rative 64; Mismatches 94; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56023 MW; 857D2E3D16B7CC1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    project;
he EMBL/GenBank/DDBJ
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Best Local Similarity 61.5
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01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF28285; AAF82385.1; -
InterPro; IPR000286; His_deacetylse.
Pfam; pF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB-LEAF.
Scharte J., Baur B.;
*Molecular cloning of histone deacetylase from Mesembryanthemum
crystallinum.";
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotytedons; core eudicots;

Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
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NLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPED--DMETRPKPRXWSG
                                                           NVPLMYLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDDSPME
                                                                                                                                               MDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSY
                                                                                                                                                                                                                                                                                     TYAGGSVGGAVKLNHGLCDIAINWAGGLHHAKKSEASGFCYVNDIVLAILELLKVHERVL
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                                      NVPLLLVGGGGYTIRYVARCWCYETGVALGFELDDKIPQHEYYEYFGPDYTLHVAPSNME
                                                                                                                       IDDESYQSLFKPIMGKVMEIFKPGAVVLQCGADSLSGDRLGCFNLS1KGHAECVKYMISF
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61.5%;
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Best Local Similarity 60.5
Matches 294; Conservative
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01-JUN-2001
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Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vannoliophyta; Liliopsida; Poales; Poaceae;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HISTONE DEACETYLASE HD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF332875; AAK01712.1; .. SEQUENCE 493 AA; 55054 NW; 0EE300BB42243Cl3 CRC64;
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Ehrhartoldeae: Oryzeae: Oryza:
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Best Local Similarity
O9VZA1
O9VZA1;
O1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
RPD3 PROTEIN,
RPD3 OR CG7471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1998) to the EMBL/GenBank/DDBJ EMBL; AF086715; AAC61494.1; FlyBase; FBgn0015805; Rpd3. InterPro; IPR000286; HIs_deacetylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Mottus R.C., Sobel R.E., "DmHDAC1.";
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Drosophila melanogaster (Fruit fly)
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PRINTS; PR01270; HDASUPER.
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                                                                                                                                                                  PRELIMINARY;
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                                                                                                          Created)
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Last annotation update)
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Bhondrai D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Borstova D., Botchan M.R., Bouck J., Bavenport L.B., Davies P.,
RA Gerbellos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorson K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gund P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
RA Hushin D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Hender K., Remington K., Stapleton M., Stupski M.P., Mense M.G.,
RA Holt R., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Hushin S.M., Moy M., Murphy L., Muzny D.M., Mense M.G.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Shen E., McChorles R., R
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Best Local 9
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InterPro: IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
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                             AFYTTDRVMTVSFHKFGDFFPGTGH1RDVGAEKGKYYALNVPLNDGMDDESFRSLFRPL1
                                                                                                               RQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEE 197
                                                                                                                                                                                                                                                     HSPEYVDFLASVSPESMGDPSAARNLRRENVGEDCPVFDGLFDFCRASAGGSIGAAVKLN 137
                                                                                                                                                                                                                                                                                                             KKRVCYYYDSDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATADEMTKF 65
                                                                                    KQASEICINWGGGLHHAKKSEASGFCYVNDIVLGILELLKYHQRVLYIDIDVHHGDGVEE
                                                                                                                                                                                                 HSDEYVRFLRSIRPDNMSEYN--KQMQRFNVGEDCPVFDGLYEFCQLSAGGSVAAAVKLN 123
Similarity
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58.6%;
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; Pred. No. 1.8e-111;
76; Mismatches 89;
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RESULT
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01-JUN-2001
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01-OCT-2000
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Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Graessle S., Dangl M., Haas H., Mair Walton J.D., Loidl P., Brosch G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20461766; PubMed=11004483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                     296
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CLRFLRSYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTL
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                                                                                           LNVPLNDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHAD
                                                                                                                                                    LKMFKRVLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGH1RDVGAEKGKYYA
                                                                                                                                                                                                           DGLFEFCGISAGGSMEGAARLNRNKCDIAVNWAGGLHHAKKSEASGFCYVNDIVLGILEL
                                                                                                                                                                                                                            DGLFDFCRASAGGS1GAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILEL
                                                                                                                                                                                                                                                                                   SIYKKMEIYRAKPASKFENTQFHTDEYIDFLSKVTPDNM--DAFAKEQSKYNVGDDCPVF
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                                                                                                                                                                                                                                                                                                                      HLHRRLEISRPSLADASDIGREHSPEYVDFLASVSPESMGDPSAARNLRRENVGEDCPVF
                                                                                                                                                                                                                                                                                                                                                           SGTSGPAGPPLDPIDLNVSGDRSKRVAYFYDSDVGNYAYVSGHPMKPHRIRMTHSLVMNY
                                                                                                                                                                                                                                                                                                                                                                                                SGISLPSGP------DGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHY
                                                                                                                                LRFKQRVLYVDIDVHHGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGELRDIGVGQGKYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR01270; HDASUPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nidulans (Aspergillus nidulans).
Fungi: Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 687 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75431 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1373; DB 3;
Pred. No. 6.2e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFC7C65352366451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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Best Local Similarity
Matches 260; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     features of the regions of clones.";
DNA Res. 7:31-63(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB023031; BAB09994.1;
InterPro; IPR000286; H15_deacetylse.
Pfam; PF00850; H1st_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-COLUMBIA;
MEDLINE-20181125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
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                                                          GAAVKLNRQDADIAINWGGGLHHAKKSEASGECYVNDIVLGILELLKMEKRVLYIDIDVH
                                                                                                                                                                                                                                                                                                                                    DGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSGVESGMATPQDASSVADEEMDTGTDVKITEAPGPEPDSEAQGTSSAAEPPS
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GGGGYTLPNVARCWCYETAIAVGEQLDNDLPGNDYMKYFRPDYKLHILPTNRQNLNTRLD
                             GGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKD
                                                                                                                                         HGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFR 250
                                                                                                                                                                                                                                                                      GRFHSPEYVDFLASVSPESMGD--PSAARNLRRFNVGEDC--PVFDGLFDFCRASAGGSI 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVDPSPMENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPP---VNRVLDEPE---DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVKYVKSFNLPTLIVGGGGYTMRNVARTWAFETGILVGDNLGSELPYNDYYEYFAPDYEL
                                                                                                                                                                                                                                                                                                                  DGGKRRVSYFYEPMIGDYYYGVNQPTKPQRIRVTHNLILSYNLHRHMEINHPDLADASDF 65
                                                                                                                          HGDEVEEAFKDTDRVMTVSFHKVGD----TGDISDYGEGKGQYYSLNAPLKDGLDDFSLR
                                                                                                                                                                                         SAAAKLNRQEADIAINWAGGMHHVKKDKASGFGYVNDVVLAILELLKSFKRVLYIEIGFP
                                                                                                                                                                                                                                                     EKFHSLEYINFLKSVTPETVTDPHPSVSENLKRFNVDVDWDGPVFHNLFDYCRAYAGGSI
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                                                                             Score 1369; DB 10;
Pred. No. 6.2e-103;
0; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          56A4FFAF9A0734AE CRC64;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Farsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               062339; 062343;
01-AUG-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z81108; CAB03240.1;
EMBL; Z81106; CAB03240.1;
EMBL; Z81106; CAB03224.1;
EMBL; Z81108; CAB03224.1;
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Pfam; PF00850; Hist_deacetyl; 1.
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nes 234; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 KRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISKPSLADASDIGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 KSRVSYYYDGDEGNEYYGQGHPMKPHRVRMTHSLIVNYGLYRKLNVMRPARASESEITRY
RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDP
                                                                  GEVMARFQPEAVVLQCGADSLAGDRLGVFNLTTYGHGKCVEYMKSFNVPLLLVGGGGYT1
                                                                                                                                 QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYT I
                                                                                                                                                                                                        AFYTTDRVMTVSFHKHGEYFPGTGDLKDVGAGSGKYYALNVPLRDGVDDVTYERIFRTIM
                                                                                                                                                                                                                                                                       AFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
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08, Last sequence update)
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Caenorhabditis.
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Best Loc
Matches
  Q9GUAB;
Q9GUAB;
01-MAR-2001
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"Expression pattern of rat histone deacetylases.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
EMBL, AF321131; AAKI1184.1; -.
SEQUENCE 428 AA; 48829 MW; 7CB448CFE33041FE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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RNVSRCWLYETAIALNQEVSDDLPLHDYFDYFIPDYKLHIKPLAALSNENTPEFIDQTIV 364
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    (TrEMBLrel.
                               PRELIMINARY;
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Best Local S
Matches 237
                                                                              Q9C1C6;
01-JUN-2001
01-JUN-2001
01-JUN-2001
HDC2.

Cochliobolus carbonum (Bipolaris zeicola)

Cochliobolus carbonum (Bipolaris zeicola)

Eukaryota; Fungi; Ascomycota; Pezizomycot.

Pleosporales; Pleosporaceae; Cochliobolus

NCBI_TaxID=5017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homolog).";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ EMBL; AF139991; AAG21919.1; -
InterPro; IPR000286; His_deacetylse.
pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryptosporidium parvum.
Eukaryota; Alveolata; Apicomplexa;
Cryptosporidiidae; Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=KSU-1;
Kasper J.K., Woods K.W., Khramtsov N.V., Upton S.J.;
"Cloning and analysis of a Cryptosporidium parvum gene enc
protein with homology to probable histone deacetylase 1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TIEMBLIE). 16,
01-JUN-2001 (TIEMBLIE). 17,
HISTONE DEACETYLASE.
                                                                    HISTONE
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                                                                                                                                                                                                                                                                                                                                           IRNVARCWCYETAVAV---GVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMER
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                                                                  2001 (TrEMBLrel. 17, Last sequence update) 2001 (TrEMBLrel. 17, Last annotation updat DEACETYLASE 2.
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Last annotation updat
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Pred. No. 2.6e-96;
0; Mismatches 95;
                        Pezizomycotina;
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01-NOV-1999 (TrEMBLrel: 12,
01-NOV-1999 (TrEMBLrel: 12,
01-JUN-2001 (TrEMBLrel: 17,
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"HDC2, a histone deacetylase gene related to RPD3, from the filamentous fungus Cochliobolus carbonum.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF349677; AAK35180.1; -
"Molecular cloning and nuclear localization homologue in Plasmodium falciparum."; Mol. Blochem. Parasitol. 99:11-19(1999). EMBL; AF091326; AAD22407.1; ...
                                                MEDLINE-99229859; PubMed-10215020;
Joshi M.B., Lin D.T., Chiang P.-H.,
Aikiwa M., Syin C.;
                                                                                                                          Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
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                                                                                         STRAIN-3D7
                                                                                                   SEQUENCE FROM N.A.
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246; Conser
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Walton J.D.;
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Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 9.5e-
86; Mismatches
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Best Local
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                           DDKPLHGYSCRGGATTD----RDSTGEDEMDDDNPEPDVNP
                                                                                      IRNTLLEQLSGLIHAPSVQFQHTPP---VNRVLDEPEDDMETRPKPRXWSGTATYESDSDD
                                                                                                                 {\tt TIRNYSRCWAYETG VYLNKH EMPDQISLNDYYDYYAPDFQLHLQPSNIPNYNSPEHLSR}
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52.4%;
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76; Mismatches
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Search completed: April 26, 2002, 17:57:28 Job time: 356 sec

Run on: OM protein - protein search, using sw model April 26, 2002, 17:57:50 ; Search time 17.07 Seconds (without alignments)
1011.666 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title: Perfect score: US-09-645-337-4 2544

MEADESGISLPSGPDGRKRR.....TGEDEMDDDNPEPDVNPPSS 471

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059

100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

DR DR DR DR DR SQ	<b>338888888888888888888888</b>	RESULT HDAC_A ID H IC
EMBL: AF014824: AAB66486.1; InterPro; IPR000286; His_deacetylse. Pfam; PF00850; Hist_deacetyl; 1. PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE. Hydrolase; Nuclear protein. SEQUENCE 501 AA; 56037 MW; C50AF5624958D6C2 CRC64; SEQUENCE 501 AA; 56037 MW; C50AF5624958D6C2 CRC64; Sequence 61.4%; Score 1561.5; DB 1; Length 501; Best Local Similarity 60.7%; Pred. No. 1.7e-121; Matches 292; Conservative 64; Mismatches 94; Indels 31; Gaps 5;	Bank/DDBJ databases. Bank/DDBJ databases. ACETYLATION OF LYSINE RESIDUES ACETYLATION OF LYSINE RESIDUES ACETYLATION OF LYSINE RESIDUES ACETYLATE (H2A, H2B, H3 AND H4) MPORTANT ROLE IN TRANSCRIPTION ON AND DEVELOPMENTAL EVENTS (B Y SIMILARITY). NE DEACETYLASE / ACUC / APHA  It is produced through a colla nformatics and the EMBL outs e. There are no restrictions chord as its content is in emoved. Usage by and for co t (See http://www.isb-sib.ch/a ch).	RESULT 1  HDAC_ARATH STANDARD; PRT; 501 AA.  1D HDAC_ARATH STANDARD; PRT; 501 AA.  AC 022446;  DT 15-UL-1998 (Rel. 36, Last sequence update)  DT 15-UL-1998 (Rel. 36, Last sequence update)  DT 15-UL-1998 (Rel. 40, Last annotation update)  DT 20-AUG-2001 (Rel. 40, Last annotation update)  DT 40-AUG-2001 (Rel. 40, Last annotation update)  DE HISTONE DEACETYLASE (HD).  OS Arabidopsis thaliana (Mouse-ear cress).  CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.  OX NOBI_TaxID-3702;

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This
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
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PRINTS; PR01271; HISDACETLASE
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15-JUL-1998 (Rel. 36, Last sequence
20-AUG-2001 (Rel. 40, Last annotati
PROBABLE HISTONE DEACETYLASE (RPD3
                                                                                          Pfam; PF00850; Hist_deacetyl;
                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
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|YDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKXYSLNVPLDDG
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                                                                                                                 IPR000286; His_deacetylse
Nuclear protein.
513 AA; 57546 MW;
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P56517;
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
HISTONE DEACETYLASE 1 (HD1).
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                     Takami
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                          SUBUNIT: FORMS A COMPLEX WITH RBAP48 (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC
                                                                                                                   SIMILARITY)
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Pred. No. 7.7e-118;
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Best Local :
                                                                                                                HDA1_MOUSE STANDARD; PRT; 482 AA 009106; P97476; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat HISTONE DEACETYLASE 1 (HD1).
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CONFLICT
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TISSUE=Fibroblast; MEDLINE=97415582; PubMed=9271381;
                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                          Mus musculus
                                                                                                       HDAC1.
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PRINTS; PR01271; HISDACETLASE.
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InterPro; IPR000286; His_deacetylse.
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                         SEQUENCE FROM N.A.
                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                       TIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIK
                                                                                                                                                                                                                                                                                                                                                                                 TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR 375
                                                                                                                                                                                                                                                                                                                                                                                                           VISKVMETFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYHSDDYIKFLRSIRPDNMSEYS--KQMQRFNVGEDCPVFDGLFEFCQLSAGGSVASAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTKRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMT 65
                                                                                                                                                                                                                                                                           SDDDD-----KPLHGYSCRGGATTDRDSTGEDEMDDDNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135
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                                                                                        (Mouse)
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                                                              Chordata;
Rodentia;
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58.8%;
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Pred. No. 2.8e
90; Mismatches
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POLY-GLU.
LT -> VM
                                                              Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82C78CE285C779D9
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82C78CE285C779D9 CRC64;
                                                                                                                               update)
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                                                                           Vertebrata; Euteleostomi;
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                                                                Muridae;
                                                                                                                                                                                                                                                   461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 480;
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EMBL; x98207; CAA66870.1; -.
EMBL; 080780, AAB68398.1; -.
MGD; MGI:108086; Hdac1.
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; His_deacetyl; 1.
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstalion the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBUNIT: FORMS A COMPLEX WITH RBAP48 (BY SIMILARITY). ALSO FORMS A COMPLEX WITH SIN3 AND SAP18 (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: NUCLEAR.
-i- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHER LEVELS IN THYMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bartl S., Taplick J., Lagger G., Khier H., Kuchler K., Seiser C.; "Identification of mouse histone deacetylase 1 as a growth factor inducible gene.";
Mol. Cell. Biol. 17:5033-5043(1997).
                                                               Hydrolase;
SEQUENCE
                                                                                               PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).

FUNCTION: ACTS AS A TRANSCRIPTIONAL REPRESSOR.

SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND TESTIS AND LOWER LEVELS IN LIVER INDUCTION: BY INTERLEUKIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY. HD SUBFAMILY
                                                           Nuclear protein.
482 AA; 55075 MW;
                                                             7F64D3C17F5E4844 CRC64
Length
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Matches Query Match Best Local Similarity 16 GRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIG 267; Conservative 57.6%; 58.9%; 77; Score 1466; DB 1; Pred. No. 1.3e-113 Mismatches 101; Indels 8 Gaps ü

Ş В 6 GTKRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMT 65

99 76 KYHSDDYIKFLRSIRPDNMSEYS -- KOMORFNVGEDCPVFDGLFEFCQLSTGGSVASAVK RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135

136

В 124 LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKWFKRVLYIDIDVHHGDGV LNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV

183 195 123

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В δÃ 184 196 EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP EEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKP 255 243

256

닭 Š 244 LIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGY VMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGY 315 303

Ş TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR

밁 304 TIRNVARCWIYETAVALDIEIPNELPYNDYFEYFGPDFKLHISPSNMINQNINEYLEKIK 363

QΥ 364 QRLFENLRMLPHAPGVQMQAIPE-DAIPEESGDEDEEDPDKRISICSSDKRIACEEEFSD

NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPR----XWSGTATYESDSD

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431 DDDKPLHGYSCRGGATTDRDSTGEDEMDDDNPE 463

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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang W.-M., Inouye C.J., Zeng Y., Bearss D., Seto E.;
"Transcriptional repression by YY1 is mediated by interaction with a
mammalian homolog of the yeast global regulator RPD3.";
Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).

1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
THE N.TERMINAL PART OF THE CORRE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HISTONE DEACETYLASE 2 (HD2) (YY1 TRANSCRIPTION FACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00850; Hist_deacetyl; 1. PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U31758; AAC52889.1; -. MGD; MGI:1097691; Hdac2. InterPro; IPR000286; H1s_deacetylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lymphoma;
MEDLINE-97075080; PubMed-8917507;
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Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Nuclear
      136 LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 SDEEGEGGRKNSSNFKKAKRVKTEDEKEKDPEE 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: FORMS A HETEROLOGOUS COMPLEX WITH YY1.
SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: FORMS TRANSCRIPTIONAL REPRESSOR COMPLEXES BY ASSOCIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).
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                                                                                                                                                                                                                               GRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIG 75
                                                                KYHSDEYIKFLRSIRPDNMSEYS - - KQMQRFNVGEDCPVFDGLFEFCQLSTGGSVAGAVK 124
                                                                                                                                                                                                GGKKKVCYYYDGDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATAEEMT 66
                                                                                                  RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                               57.6%;
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8; Mismatches
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Pred. No. 1.4e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HDA1_HUMAN STANDARD; PRT; 482 AA. 013547; 092534; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HISTONE DEACETYLASE 1 (HD1).
                                                                                                                                                                                                                     *Isolation and mapping of a human gene (RPD3L1) that is homologous to RPD3, a transcription factor in Saccharomyces cerevisiae.*;
Cytogenet, Cell Genet, 73:130-133(1996).
-:- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORPANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS.
-:- SUBUNIT: FORMS A COMPLEX WITH RBAP48 AND ALSO WITH THE HISTONE ACETYLTRANSFERASE P/CAF AND THE ADAPTATOR PROTEIN P300, ALSO FORMS A COMPLEX WITH SAPELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A mammalian histone deacetylase related regulator Rpd3p."; Science 272:408-411(1996).
                                                                                                                                                    -:- SUBCELLULAR LOCATION: NUCLEAR.
-:- TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHER LEVELS IN HEART,
-PANCYREAS AND TESSTIS, AND LOWER LEVELS IN KIDNEY AND ERAIN.
-:- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96185499; PubMed=8602529; Taunton J., Hassig C.A., Schreiber S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                Akiyama T., Nakamura Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDAC1 OR RPD3L1
                                                                                                                                                                                                                                                                                                                                                                                                                 Furukawa Y., Kawakami T., Sudo K., Inazawa J., Matsumine A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96244606; PubMed=8646880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   fung;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
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SEQUENCE
                                                                                                                                                                                                      HD11_XENLA STANDARD; PRT; 480 AA. 091695; 091695; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE HISTONE DEACETYLASE 1-1 (HD1) (MATERNALLY-EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U50079; AAC50475.1;
EMBL; D50405; BAA08909.1;
MIM; 601241; --
             Ladomery M.R., Lyons S., Sommerville J.;
"Xenopus HDm, a maternally expressed histone deacetylase,
an ancient family of acetyl-metabolizing enzymes.";
Gene 198:275-280(1997).
                                                                                                                                                  HISTONE DEACETYLASE) (HDM) (AB21).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                    XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Nuclear protein.
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PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00850; Hist_deacetyl; 1.
                                                                  MEDLINE-98036059; PubMed-9370292;
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                         Xenopodinae;
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FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES
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55103 MW; 4D35B7C1ED7838D6 CRC64;
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Pred. No. 2.5e-113;
'9; Mismatches 80;
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DOMAIN 299 302
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PRINTS; PR01271; HISDACETLASE.
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SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

TISSUE SPECIFICITY: OOCYTE.

TISSUE SPECIFICITY: OOCYTE.

DEVELOPMENTAL STAGE: ACCUMULATES IN PREVITELLOGENIC OOCYTES AND INTO EARLY EMBRYOGENESIS. DECLINES THROUGHOUT OOGENESIS AND INTO EARLY EMBRYOGENESIS. DECLINES THROUGH GASTRULA TO NEUBULA. NOT DETECTABLE BETWEEN NEURULA AND TAILBUD, NOR IN ADULT TISSUES OTHER THAN OVARY.

SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA FAMILY. HD SUBFAMILY 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNRQDADIAINWGGGLHHAKKSFASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV 195
                                                        LHGYSCRGGATTDRDSTGEDEMDDDNPE 463
                                                                                                                       QRLFENLRMLPHAPGVQMQAVAE-
                                                                                                                                                   NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP
                                                                                                                                                                                                                                        TIRNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNONTNEYLEKIK
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-SIR---SSDKRIACDEEFSDSEDE
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Pred. No. 7.7e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLY.; 7B831822235DADB5 CRC64;
                                                                                                                    --DSIHDD
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   426
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RESULT 8
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HD12\_XENLA 042227;

STANDARD;

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Best Local S
Matches 263
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PATTERION D., Wolffe A.P.;

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; His_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE HISTONE DEACETYLASE 1-2 (HD1) (RPD3 HOMOLOG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Nuclear protein.
DOMAIN 299 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRKRRVSYPYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIG 75
                                                                                                                                                                                                                                         LIOKVMEVYOPEAVVLOCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGY
                                                                               NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP
                                                                                                                    TIRNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIK
                                                                                                                                                          TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR
                                                                                                                                                                                                   VMTKVMENFQPSAVVLQCGADSLSGDRLGCFNLTIKGHAKCVEFIKTFNLPMLMLGGGGGY
                                                                                                                                                                                                                                                                                   EEAFYTTDRVMSVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKP
                                                                                                                                                                                                                                                                                                            EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP
                                                                                                                                                                                                                                                                                                                                                                LNKQQTDISVNWSGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVVYIDIDIHHGDGV
                                                                                                                                                                                                                                                                                                                                                                                                 LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                             KYHSDDYIKFLRSIRPDNMSEYS - - KOMORFNVGEDCPVFDGLFEFCQLSTGGSVASAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTKKKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKASAEEMT
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                                                                                                                                                                                                                          54892 MW;
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58.7%;
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Pred. No. 1.4
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CA92DE34D36E39E8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson C.A., White D., O'Neill L.P., Turner B.M.;
Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                      EMBL; AF026949; AAC23917.1; FlyBase; FBgn0015805; Rpd3
                                                                                                                                                                                                                                                                                                                                     use
                                                                                                                                                       CONFLICT
                                                                                                                                                                                 PRINTS; PR01271;
                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                           Pfam; PF00850; Hist_deacetyl;
                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                          modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de Rubertis F., Kadosh D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97113416; PubMed=8955276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPD3 OR HDAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE HISTONE DEACETYLASE (HD) (DRPD3).
                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                           InterPro; IPR000286; His_deacetylse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The histone deacetylase RPD3 counteracts genomic 
Drosophila and yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405
                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL) SIMILARITY: BELONGS TO THE HISTONE DEACET FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS () SIMILARITY). IN DROSOHILA, IT IS INVOLVED IN POSITION-EFFECT VARIEGATION (PEV) AND IS DIRECTLY INVOLVED IN COUNTERACTING GENOME SILENCING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I---SIR---SSDKRIACDEEFSDSEDE
                                                                                                                                                                                                                                                                   Y09258; CAA70455.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nila and yeast.";
384:589-591(1996).
                                                                                                                                                                                               PR01270; HDASUPER
                                                                                                                                                                                                                                                                                                                       non-profit institutions as long and this statement is not removed.
                                                      50
66
96
105
295
295
370
506
                                                                                                                                                                     Nuclear
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                                                                                                                                                                                 HISDACETLASE
                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                     institutions as long as its content
57.1%;
57.9%;
                                                        58183 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     THE HISTONE DEACETYLASE /
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                                                   DI -> EIY (IN REF. 2).
C -> S (IN REF. 2).
D -> N (IN REF. 2).
E -> D (IN REF. 2).
V -> VV (IN REF. 2).
L -> V (IN REF. 2).
S -> T (IN REF. 2).
D02EA3DBD3C64688 CRC64
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18

KRRVSYFYEPTIGDYYYGOGHPMKPHRIRMAHSLIIHYHLHRRLEISKPSLADASDIGKF 77

Query Best [ Matches

Local Similarity nes 270; Conserv

Conservative

77;

Pred. No. 1.507; Mismatches Score 1453.5;

.5e-DΒ

Length

29;

Gaps

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RESULT 10
HDA2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q92769;
15-JUL-1998
15-JUL-1998
20-AUG-2001
                                                                                                                                                                                                                                                                  Yang W.-M., Inouye C.J., Zeng Y., Bearss D., Seto E.;
"Transcriptional repression by YY1 is mediated by interaction with a mammalian homolog of the yeast global regulator RPD3.";
Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).
-i- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Breast
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97075080; PubMed=8917507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                       WITH MAD, SIN3, YY1 AND N-COR.
SUBUNIT: FORMS A HETEROLOGOUS COMPLEX AT LEAST WITH YY1
                                                                                                                                                                                                                       SIMILARITY).
FUNCTION: FORMS TRANSCRIPTIONAL REPRESSOR COMPLEXES
                                                                                                                          SIMILARITY:
                                                                                                        FAMILY. HD SUBFAMILY
                                                                                                                                                        TISSUE
                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                        REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSDSEDEGE-----GGRRDNRSYKGQRKRPRLDKDTNSNKASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFYTTDRYMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLERPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIRNT
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-1998 (Rel. 36, I
-2001 (Rel. 40, I
E DEACETYLASE 2 (
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                                                                                                                        BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
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P56518;
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15-JUL-1998 (Rel. 36,
20-AUG-2001 (Rel. 40,
HISTONE DEACETYLASE 1
                                                                                                                                                                                                                                                                                                   STRPU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U31814
MIM; 605164;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES CONTINUES OF THE UNITED HAVE AND HAVE THE UNITED DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).
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                                                                                                                           NCBI_TaxID=7668;
                                                                                                                                        Strongylocentrotus
                                                                                                                                                                    Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; E
                                                                                                                                                                                                   HDAC1
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                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                      LHGYSCRGGATTDRDSTGEDEMDDDNPE 463
                                                                                                                                                                                                                                                                                                                                                                                                                  QRLFENLRMLPHAPGVQMQAIPE----DAVHED----
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                                                                                                                                                                                                                                                                                    STANDARD;
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59.6%;
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Last annotation
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                                                                                                                                                         Echinacea;
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                                                                                                                                                       Echinoida; Strongylocentrotidae;
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                                                                                                                                                                      Echinozoa
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RESULT 12
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Best Local S
Matches 267
                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HISTONE DEACETYLASE 2 (HD2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00850; Hist_deacetyl; 1. PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentities requires a license agreement (See http://www.isb-sib.ch/arerement to license@isb-sib.ch).
                                           Eukaryota; Metazoa;
Archosauria; Aves; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
NCBI_TaxID-9031;
                                                                         Gallus gallus (Chicken).
                                                                                                                                                                       HDA2_CHICK P56519;
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                                                                                            HDAC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRKRRVSYFYEPTIGDYYYGGGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIG
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                                                                                                                                                                                                                                                                                               DSDDD-DKPLHGYSCRGGATTDRDSTGEDEMDDDNP--EPDVNPPSS 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV
                                                                                                                                                                                                                                                                  DSEDEGETRLPG---EGGRRDHRSHKAKRSKIDDSPGKEADKEAKSS 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                       STANDARD;
                                             Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64078 MW;
                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.7%; Score 1441.5; DB 1; Length 576; 57.2%; Pred. No. 1.7e-111;
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                                             Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B3D11A844A2088E9 CRC64;
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                                           Phasianinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-:- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON

-:- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON

--- TEBMINLAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).

--- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

--- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on in
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DOMAIN 300 303
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PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Takami Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00850; Hist_deacetyl;
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I---SIR---ASDKRIACDEEFSDSEDE
                                                                                                                                                                             TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHGYSCRGGATTDRDSTGEDEMDDDNPE
                                                                                  QRLFENLRMLPHAPGVQMQAIPE----DAVHED
                                                                                                                   NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP 435
                                                                                                                                                             TIRNVARCWTYETAVALDCEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTPEYMEKIK
                                                                                                                                                                                                                                    IISKVMEMYQPSAVVLQCGADSLSGDRLGCFNLTVKGHAKCVEVVKTFNLPLLMLGGGGY
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                                                                                                                                                                                                                                                                                                              EEAFYTTDRVMTVSEVSMVNNFPGTGDLRDIGAGKGKYYAVNFPMRDGIDDESYGQIFKP
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                                                                                                                                                                                                                                                                                                                                                                                     LNRQQTDMAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV
                                                                                                                                                                                                                                                                                                                                                                                                                      LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGKKKYCYYYDGDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATAEEMT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000286; His_deacetylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 AA;
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RESULT 13
HDA1\_CAEEL
ID HDA1\_CAEEL
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STANDARD; 36, 36,

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Query Match
Best Local S
Matches 262
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-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORPANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z81486; CAB03984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDA-1 OR C53A5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE HISTONE DEACETYLASE 1.
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InterPro; IPR000286; His_deacetylse
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SUBCELLULAR LOCATION: NUCLEAR SIMILARITY: BELONGS TO THE HIS
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                                                                                                              QSIFKPIMTKVMERFDPCAVVLQCGADSLNGDRLGPFNLTLKGHGECARFFRSYNVPLMM
                                                                                                                                                                                                                       HHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESF
                                                                                                                                                                                                                                                                LAAATKLNKQKVDIAINWMGGLHHAKKSEASGFCYTNDIVLGILELLKYHKRVLYVDIDV
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                 DDDDKPLHGYSCRGGATTDRD-STGEDEMDDDNPEPD
                                                                    DMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDS
                                                                                                                                                                   HHGDGVEEAFYTTDRVMTVSFHKYGDFFPGTGDLKDIGAGKGKLYSVNVPLRDGITDVSY
                                                                                                                                                                                                                                                                                          IGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDV
                                                                                                                                                                                                                                                                                                                  SFEDMTRFHSDEYMTFLKSANPDNL--KSFNKQMLKFNVGEDCPLFDGLYEFCQLSSGGS
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                                         MLAKLQTDVIANLEQLTFVPSVQMRPIP--EDALSALNDD--
                                                                                                VGGGGYTPRNVARCWTYETSIAVDKEVPNELPYNDYFEYFGPNYRLHIESSNAANENSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein.
461 AA; 52137 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1359.5; DB 1
Pred. No. 7.6e-105;
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STONE DEACETYLASE
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01-OCT-1993
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Last annotation update)
HISTONE DEACETYLASE RPD3 (TRANSCRIPTIONAL REGULATORY PROTEIN RPD3).
RPD3 OR SDI2 OR YNL330C OR NO305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95373280; PubMed-7645347;
Maftahi M., Nicaud J., Levesque H., Gaillardin C.;
"Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the RPD3, PAS8 and KREI loci, five new open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C / FY1679;
van Dyck L., Pascual-Ahuir A.,
Submitted (DEC-1994) to the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grunstein M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE=97121415; PubMed=8962081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=92049362; PubMed=1944291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-201 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D3 encodes a second factor required to achieve maximum positive negative transcriptional states in Saccharomyces cerevisiae."; Cell. Biol. 11:6317-6327(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATION AND CELL CYCLE PROGRESSION. REQUIRED FOR BOTH FULL TRANSCRIPTION REPRESSION AND ACTIVATION OF MANY GENES INCLUDING CELL TYPE-SPECIFIC GENES (STE6, TY2 AND HO), CELL DIFFERNTIATION-SPECIFIC GENES (SPO13), GENES THAT RESPOND TO EXTERNAL SIGNALS
                                                                                                                                                                                                                                                                                                                                  FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR SIMILARITY:
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HELIX PROTEIN SIN3/RF
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$66438;

$83226;

$246259;

$71605;

$71606;
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                   AAB20328.1;
CAA58228.1;
CAA86368.1;
CAA96262.1;
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BELONGS TO
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SIN3/RPD1. IN
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O THE HISTONE DEACETYLASE /
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Matches 238
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15-JUL-1998 (Rel. 36, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
HISTONE DEACETYLASE 3 (HD3).
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P56520;
                                                                                                                                                                                                                                                                                                                                                                                 CHICK
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SGD; S0005274; RPD3.
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Gailiformes; Phasianidae; Phasiani
                                                                                                                                                                            Takami Y
                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
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nes 238; Conserv
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                                                     SIMILARITY: BELONGS TO THE HISTONE FAMILY. HD SUBFAMILY 1.
                                                                                 SUBCELLULAR LOCATION: NUCLEAR
                                                                                            SIMILARITY)
                                                                                                           REGULATION, CELL CYCLE PROGRESSION
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433 AA; 48904 N
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57.9%;
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Pred. No. 2.5e-102;
4; Mismatches 94;
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EMBL outstation -
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Best Local S
Matches 237
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modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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PRINTS; PR01271; HISDACETLASE.
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GDHDND
                                SDSDDD
                                                                 TIFENLKMLNHAPSVQIHDVPSDLLSYDRT-DEPDPEERGSEENYSRPE---
                                                                                                 TLLEGLSGLIHAPSVQFQHTP----PVNRVLDEPE-----DDMETRPKPRXWSGTATYE
                                                                                                                                      RNVARCWTYETSLLVDEAISEELPYSEYFEYFAPDFTLHPDVSTKIENQNSRQYLDQIRQ
                                                                                                                                                                    RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSP-MENLNTPKDMERIRN
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                                                                                                                                                                                                                                         QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
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237; Conservative
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421
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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Search completed: April 26, 2002, 17:57:52 Job time: 335 sec

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Result
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Maximum DB seq length: 2000000000
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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### ALIGNMENTS

Qy 184 YIDIDVHHGDGVEEAFYTTDRY	Qy 4 DESGISLPSGPDGRKRRVSYFYEPTIGDYYY	Genetics: A; Genet Los: A; Genet Los: A; Genet ATSP: F20D10.250 A; Map position: A; Throns: 176,3; 323/3; 400/3; 424/2; 443/3; 467/3 A; Introns: 176,3; 323/3; 400/3; 424/2; 443/3; 467/3 C; Superfamily: RPD3 protein: RPD3/acuC homology C; Keywords: hydrolase F; 21-320/Domain: RPD3/acuC homology <rah>  Query Match Best Local Similarity 60.7%; Pred. No. 2.8e-116; Matches 292; Conservative 64; Mismatches 94; Ind</rah>	RESULT 1  105640  histone deacetylase (EC 3.5.1) F20D10.250 - Arabidopsis histone deacetylase (EC 3.5.1) F20D10.250  N; Alternate names: protein F20D10.250  C. Species: Arabidopsis thaliana (mouse-ear cress) C. Species: Arabidopsis thaliana (mouse-ear cress) C. Species: T05640  C. Accession: T05640  R. Hevan, M.: Wedler, H.; Kutzner, M.; Wambutt, R.; Bancro submitted to the Protein Sequence Database, February 1999 A; Reference number: Z15420  A; Accession: T05640  A; Molecule type: DNA  A; Residues: 1-501 < BEV> A; Cross; references: EMBL: AL035538; GSPDB:GN00062; ATSP:F2  A; Cross; references: EMBL: AL035538; GSPDB:GN00062; ATSP:F2
	DESGISLPSGPDGRKRRVSYFYEPTIGDYYYGOGHPMKPHRIRMAHSLIIHYHLHRRLEI 63	# 424/2; 443/3; 467/3  ###################################	RESULT 1 1705540 histone deacetylase (EC 3.5.1) F20D10.250 - Arabidopsis thaliana histone deacetylase (EC 3.5.1) F20D10.250 - Arabidopsis thaliana N;Alternate names: protein F20D10.250 C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 23-Apr-1999 *Sequence_revision 23-Apr-1999 *text_change 12-Nov-1999 C;Accession: T05640 R:Bevan, M.: Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Submitted to the Protein Sequence Database, February 1999 A;Reference number: Z15420 A;Accession: T05640 A;Accession: T05640 A;Molecule type: DNA A;Residues: 1-501 (SBEV) A;Cross_references: EMBL:AL035538; GSPDB:GN00062; ATSP_F20D10.250
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A; Gene:
C; Superf
C; Keywor
F; 27-325
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A:Title: Identification and characterisation of an RPD3 homologue from maize (2 A:Title: need number: 214321; MUID:98307342
A:Accession: T01413
A:Accession: T01413
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-513 <ROS
A:Cross-references: EMBD:AF035815; NID:92665839; PIDN:AAC50038.1; PID:92665840
A:Experimental source: strain W22
C:Genetics:
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C; Species: Zea ma
C; Date: 12-Feb-19
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;Rossi, V.; Hartings, H.; Motto, M.
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;Keywords: hydrolase
;27-325/bomain: RPD3/acuC homology <RAH>
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Best Local
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                                                                                                                                                         SYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSP
                                                                                                                                                                                                            DGIDDESYQSLFKPIMGKVMEVFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVRYMR
                                                                                                                                                                                                                              DGMDDESFRSLFRPLIQXVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLR
                                                                                                                                                                                                                                                                               VLYVDIDIHHGDGVEEAFYTTDRVMTVSFHKFGDYFPGTGDIRDIGHSKGKYYSLNVPLD
                                                                                                                                                                                                                                                                                                                                                                                  CRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKR 181
                                                                                                                                                                                                                                                                                                                                                                                                                    QVYRPNPARERELCRFHAEEYINFLRSVTPETQQD--QIRLLKRFNVGEECPVLDGLYSF
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                                                                                                   MENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRV--LDEPEDDMETRPKPRXW
                                                                                                                                       SFNVPLLLLLGGGGYTIRNVARCWCYETGVALGQEPEDKMPVNEYYEYFGPDYTLHVAPSN
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-DSDMEVDD 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1517.5; DB 2;
Pred. No. 7.6e-113;
Pred. No. 7.6e-113;
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A:Gene: CESP:C53A5.3 A:Man position: 5

C; Genetics:

A; Experimental source:

clone

C53A5

A; Molecule type: DNA A; Residues: 1-461 <WIL>

A; Status: preliminary; translated

from

GB/EMBL/DDBJ

A; Accession: T20163

R; Mortimore,

Accession:

A;Cross-references: EMBL:Z81486; PIDN:CAB03984.1; GSPDB:GN00023; CESP:C53A5.3

hypothetical protein C53A5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000

submitted to the EMBL Data Library, November A; Reference number: Z19232

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RESULT 3
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SCOURT 3
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RPD3 protein homolog - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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R;Ladomery, M.R.; Lyons, S.; Sommerville, J.
submitted to the EMBL Data Library, December 1994
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A; Residues: 1-480 <LAD>
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A;Accession: S60381
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Best Local Similarity 59.4%; Pred. No. 4.9e-108;
405 I---SIR---SSDKRIACDEEFSDSEDE 426
                                                                                                                                      376
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                                                                                                                                                                                                                                                                          244 VMSKVMEMFQPSAVVLQCGADSLSGDRLGCFNLTIKGHAKCVEFIKTFNLPLLMLGGGGY
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                                           LHGYSCRGGATTDRDSTGEDEMDDDNPE 463
                                                                                                                                                                                                                                                                                                                      LIOKVMEVYOPEAVVLOCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGY
                                                                                                                                                                               TIRNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIK
                                                                                           QRLFENLRMLPHAPGVQMQAVAE-----DSIHDD------SG----EEDEDDPDKR
                                                                                                                                                                                                                          TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR
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                                                                                                                                    NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDUUDKP
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R;Nicand, J.J.

R;Nicand, J.J.

submitted to the EMBL Data Library,

submitted to Sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001
C;Accession: S22284; S51336; S51285; S55859; S57393; S63313; S63311
R;Vidal, M.; Gaber, R.F.
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A;Title: RPD3 encodes a second factor required
A;Reference number: S22284; MUID:92049362
A;Accession: S22284
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C:Superfamily: RPD3 protein; RPD3/acuC homology
                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X83226; NID:g642335; PIDN:CAA58228.1; PID:g642338
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-433 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S51334
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                                                                                              A; Accession: S51285
                                                                                                                                    A; Reference number: S51285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           icated gene for a putative aryl-alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, December 1994
A; Description: A 8.2 kb DNA segment from chromosome XIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:S66438; NID:g238961; PIDN:AAB20328.1; PID:g238962
R;van Dyck, L.; Pascual-Ahuir, A.; Goffeau, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: not compared with conceptual translation
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Molecule type: DNA ; Molecule 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 DDDDKPLHGYSCRGGATTDRD-STGEDEMDDDNPEPD 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 MLAKLQTDVIANLEQLTFVPSVQMRPIP--EDALSALNDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 QSIFKPIMTKVMERFDPCAVVLQCGADSLNGDRLGPFNLTLKGHGECARFFRSYNVPLMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 SFEDMTRFHSDEYMTFLKSANPDNL--KSFNKQMLKFNVGEDCPLFDGLYEFCQLSSGGS
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Pred. No. 2.4e-100;
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                                                                                                                                                                           a 13.9 Kb fragment of yeast chromosome XIV identific
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A; Description: transcription regulation
C; Superfamily: RPD3 protein; RPD3/acuc homology
C; Keywords: nucleus; transcription regulation
F; 23-322/Domain: RPD3/acuC homology < RAH1>
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994
R;Coster F: Jonniaux, J.L.; Goffeau, A.; Purnelle, B.; Van Dyck, L.
submitted to the Protein sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast 11, 567-572, 1995
A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome
A;Reference number: S55859; MUID:95373280
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A;Cross-references: SGD:S0005274; MIPS:YNL330c
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A; Residues: 1-433 <V
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Yeast 11, 9
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
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A; Residues: 1-201 <M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z71606; GSPDB:GN00014; MIPS:YNL330cA;Experimental source: strain S288C
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A; Residues: 1-201 <MAW>
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A; Residues: 1-433 <COS>
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                                                      196
258 QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
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nes 238; Conser
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                                                                                                    AFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
                                                                                                                                                                                                                                                         HTDEYIDFLSRVTPDNL--EMFKRESVKFNVGDDCPVFDGLYEYCSISGGGSMEGAARLN
                                                                                                                                                                                                                                                                                                                                                                  KRRVAYFYDADVGNYAYGAGHPMKPHRIRMAHSLIMNYGLYKKMEIYRAKPATKQEMCQF
                                                AFYTTDRVMTCSFHKYGEFFPGTGELRDIGVGAGKNYAVNVPLRDGIDDATYRSVFEPVI
                                                                                                                                                       RGKCDVAVNYAGGLHHAKKSEASGFCYLNDIVLGIIELLRYHPRVLYIDIDVHHGDGVEE
                                                                                                                                                                                  RQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEE
                                                                                                                                                                                                                                                                                                            HSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
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hypothetical protein R06C1.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Coenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change C;Accession: T23963; T24071 R;Kershaw, J. Submitted to the EMBL Data Library, October 1996 Submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, October 1996
A; Reference number: 219837
A; Accession: T24071
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-465 < WIZ>
A; Cross-references: EMBL: Z81108; PIDN: CABO3240.1; GSPDB: GN00019; GESP: R06C1.1
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A;Accession: T23963
A;Status: preliminary; translated from
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A:Introns: 53/3; 212/1; 279/1; 326/1
C:Superfamily: RPD3 protein; RPD3/ac
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A:Gene: CESP:R06Cl.1
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A; Residues: 1-465 <WIL>
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                                                                                                                                                                                           QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
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                                     TLLEQLSGLIHAPSVQFQ
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ALLENLKOLPHVPSVQMQ
                                                                                 RNVSRCWLYETAIALNQEVSDDLPLHDYFDYFIPDYKLHIKPLAALSNFNTPEFIDQTIV
                                                                                                                           RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDP-SPMENLNTPKDMERIRN
                                                                                                                                                                                                                                                       AFYTTDRVMTVSFHKHGEYFPGTGDLKDVGAGSGKYYALNVPLRDGVDDVTYERIFRTIM
                                                                                                                                                                                                                                                                                             AFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
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61.9%;
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Pred. No. 4.8e-96;
7; Mismatches 74;
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RESULT 7

JC7102
histone deacetylase (EC 3.5.1.-) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 *sequence_revision 03-Dec-1999 *text_change 11-May-2000
C:Accession: JC7102
R:Accession: U:: Hoelzer, D:: Bucala, R:: Verdin, E.
Biochem. Biophys. Res. Commun. 263, 482-490, 1999
A:Title: Cloning and characterization of the murine histone deacetylase (HDF A:Reference number: JC7102: MUID:99423490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Map position: 18B3
A:Introns: 19/1; 46/3; 94/2; 121/3; 140/3; 159/2; 204/1; 231/1; 252/3; 277/2; 307/2; C:Superfamily: RPD3 protein: RPD3/acuC homology C:Keywords: hydrolase; phosphoprotein E:7-307/Domain: RPD3/acuC homology <RAH1>
F:232,282,404/Binding site: phosphate (Tyr) (covalent) #status predicted
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A; Residues: 1-424 < MAH>
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421 D
                                                                                 361 TIFENLKMLNHAPSVQIHDVPADLLTYDRTDEADAEERGPEENYSRPEAPNEFYDGDHDN
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hes 235; Conserv
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                                                                                                                                                                     OKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
                                                                                                                        TLLEQLSGLIHAPSVQFQHTPPVNRVLDEPED-DNETRPKPRXWSGTAT----YESDSDD
                                                                                                                                                                                                              RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSP-MENLNTPKDMERIRN
                                                                                                                                                                                                                                                          SQVVDFYQPTCIVLQCGADSLGCDRLGCFNLSIRGHGECVEYVKSFNIPLLVLGGGGYTV
                                                                                                                                                                                                                                                                                                                                              {\tt FYLTDRVMTVSFHKYGNYFFPGTGDMYEVGAESGRYYCLNVPLRDGIDDQSYKHLFQPVI}
                                                                                                                                                                                                                                                                                                                                                                                         FYTTDRVMTVSFHKFGD-FFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
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421
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R;Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R.; Utku, N.; Gullans, Biochem. Biophys. Res. Commun. 242, 648-652, 1998
A;Title: Differential display cloning of a novel human histone deacetylase (HDAC3) c A;Reference number: JC5834; MUID:98125547
A;Accession: JC5834

A; Status:

nucleic

acid

sequence not

shown

histone deacetylase (EC 3.5.1.-) 3 - human C:Species: Homo sapiens (man) C:Date: 05-Mar-1998 #sequence\_revision 13-Mar-1998 #text\_change 12-Nov-1999

Accession: JC5834

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histone deacetylase (EC 3.5.1.) - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: cryptic loci regulator protein clr6
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_change 21-Jul-2000
C;Accession: T40300; T43796
R;Lync, M; Wood, V; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl, submitted to the EMBL Data Library, May 1998
A;Reference number: Z21919
A;Accession: T40300
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A; Residues: 1-428 <DAN>
A; Residues: 1-428 <DAN>
A; Cross-references: GB:U66914; NID:g2934900; PIDN:AAC52038.1; PID:g2326173
C:Comment: This enzyme plays a role in multiple and complex cellular pathways of gets for the treatment of cancer and autoimmunity.
C:Superfamily: RPD3 protein; RPD3/acuC homology
                                                                                                      A;Cross-references: EMBL:AL023589; PIDN:CAA19053.1; GSPDB:GN00067; SPDB:SPBC36.
A;Experimental source: strain 972h-; cosmid c36
R;Grewal, S.I.; Bonaduce, M.J.; Klar, A.J.
Genetics 150, 563-576, 1998
A;Tittle: Histone deacetylase homologs regulate epigenetic inheritance of transc A;Reference number: 222685; MUID:98429513
A;Accession: T43796
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-405 <GRE>
A;Cross-references: EMBL:AF064206; NID:g4159996; PIDN:AAD05211.1; PID:g4159997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYLTDRVMTVSFHKYGNYFFPGTGDMYEVGAESGRYYCLNVPLRDGIDDQSYKHLFQPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEDYIDFLQRVSPTNM---QGFTKSLNAFNVGDDCPVFPGLFEFCSRYTGASLQGATQLNN
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Pred. No. 1.7e-94;
Pred. No. 1.7e-94; Indels
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81

VEFWVAGDVGSVYFGPNHPMKPHRLCMTHHLILAYGLHSKMEVYRPHKAYPIEMAQFHSP 63
EYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKLNROD 140

Qy

21 VSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIGRFHSP 80

b

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A;Experimental source: strain 972
c;Genetics:
A;Gene: clr6; SPBC36.05c
A;Map position: 2
A;Map position: 2
A;Introns: 14/1; 34/3; 51/3; 91/1; 101/2; 116/1;
C;Superfamily: RPD3 protein; RPD3/acuC homology
C;Keywords: hydrolase; transcription regulation
                                                                                                    A:Introns: 47/3; 87/1; 112/1; 185/2; 206/3; 237/3; A:Note: T18B22.80 C:Superfamily: RPD3 protein; RPD3/acuC homology
                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T18B22.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 *sequence_revision 20-Apr-2000 *text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                     A; Reference number: Z24467
A; Accession: T47443
                                                                                                                                                                                                                                                                                                                                                             R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, submitted to the Protein Sequence Database, February 2000
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                                                                                                                                                                  A; Map position: 3
                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                               A; Experimental source: cultivar Columbia; BAC clone T18822
                                                                                                                                                                                                                                     A; Cross-references: EMBL:AL138652
                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-419 < JOR>
                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T47443
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Best Local :
                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 FFYTTDRVMTCSFHKFGEYFPGTGHIKDTGIGTGKNYAVNVPLRDGIDDESYESVFKPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 HTDEYIEFLWRVTPDTM--EKFQPHQLKFNVGDDCPVFDGLYEFCSISAGGSIGAAQELN
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Conservative
                 47.4%; Score 1207; DB 2; 53.4%; Pred. No. 2.8e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.1%; Score 1275; DB 2; 59.5%; Pred. No. 1.1e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382
71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
109;
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                                                                                                                                                270/1; 286/3; 317/1; 340/3; 373/3;
                                     Length 419;
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Indels
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16;
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Gaps
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histone deacetylase (EC 3.5.1.-) - fission yeast (Schizosaccharomyces pombe N;Alternate names: Phd1 protein C;Species: Schizosaccharomyces pombe C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: T11643; T43300
                                                                                                                                                                                                                                                                           A;Description: involved in the meiotic ce
C;Superfamily: RPD3 protein; RPD3/acuC ho
C;Keywords: hydrolase
F;30-330/Domain: RPD3/acuC homology <RAC>
                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: hdal; Phdl; SPAC3G9.07c
A;Map position: IL
C;Function:
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A;Accession: T43300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T11643; T43300
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
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A;Molecule type: DNA
A;Residues; 1-434 <KIM>
A;Cross-references: EMBL:AB008888; NID:g2641698; PIDN:BAA23598.1; PID:g2641699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:ALO21046
R;Kim, Y.B.; Honda, A.; Yoshida, M.; Horinouchi, FEBS Lett. 436, 193-196, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-434 <WOO>
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A;Accession: T11643
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    FHREDYLDFLKRVTPDNA--EQFADKFQQFNIGDDCPVFDGTYEFSQRSAGASLDASRKL
                                                                                                          RKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIGR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQLSGLIHAPSVQFQHTPPVNRVLDEPED-----DMETRPKPRXWSGTATYESDSDD 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARCWTVETGILLDTELPNEIPENDYIKYFAPDFSLKIPGGHIENLNTKSYISSIKVQIL
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                                                                                     QKKRYTYHLDEQVGNYHYGDKHPMKPHRITITNHLVMGYGLHNKMSVFSPRMATFGEMSE
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                                            FHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKL 136
                                                                                                                                                                          Conservative
                                                                                                                                                                                         44.9%;
                                                                                                                                                                      ; Score 1143.5; DB 2; Length
; Pred. No. 3.3e-83;
73; Mismatches 100; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C08B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 31-Jan-2000
C;Accession: T19067
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A; Introns: 45/1;
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A; Residues: 1-507 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Sims, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone C08B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z46676; PIDN:CAA86662.1; GSPDB:GN00020; CESP:C08B11.2
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                                            GKPLMVLGGGGYTLRNVARCWALETGVILGLRMDDEIPGTSLYSHYFTPRLLRPNLVPKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNDEI 1EPDGADVKKRNVAYYYHKDVGHFHYGQLHPMKPQRLVVCNDLVVSYEMPKYMTV
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ENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGT
                                                                  NVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNE-YFEYFGPDYTLHVDPSPM
                                                                                                                         IRDEPYLKLFESVISGVEENENPEAIVLQCGSDSLCEDRLGQFALSFNAHARAVKYVKSL
                                                                                                                                                                    MDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSY
                                                                                                                                                                                                               Y IDIDIHHGDGVQEAFNNSDRVMTVSFHRFGQYFPGSGSIMDKGVGPGKYFAINVPLMAA
                                                                                                                                                                                                                                                                                                                                                                                                                      SRPSLADASDIGRFHSPEYYDFLASYSPESMGDPSAARNLRRFNYGEDCPYFDGLFDFCR 123
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Pred. No. 5.3e-75;
Pred. No. 5.3e-75;
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372

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252

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192

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7;

A.L.; Graham,

D.E.;

not shown

Gaps

14;

89

7.1

148

247

265

355

301

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probable transcription regulator YGL194c - yeast (Saccharomyces cerevisiae)
W,Alternate names: hypothetical protein G1330
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000
C;Accession: S64211; S62051
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C:Superfamily: RPD3 protein; RPD3/acuC homology
F:30-331/Domain: RPD3/acuC homology <RAH1>
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A; Gene: SGD: HOS2
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R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, submitted to the Protein Sequence Database, May 1996
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R:Coglievina, M.; Delneri, D.; Zaccaria, P.; Klima, R.; Bertani, I.; Bruschi, submitted to the EMBL Data Library, September 1995
A:Description: A 6.7 Kb fragment from chromosome VII of Saccharomyces cerevisi
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A; Cross-references: EMBL: Z72716; NID:g1322818; PIDN: CAA96906.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-351,'HSGTHS',358,'RITHFI',365-452 <COG>
A;Cross references: EMBL:X91837; NID:gl177627; PIDN:CAA62950.1;
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A; Accession: S62051
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A; Accession: S64211
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    RIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDD 432
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                                               NVSRLWTYETGILNDVLLPEDIPEDIPFRDSFGPDYSLY - - - - PMLDDLYENKNSKKLLE
                                                                                         NVARCWCYETAVAVGVEPDNKLPYNEYF-EYFGPDYTLHVDPSPM-----ENLNTPKDME
                                                                                                                                      PLIMTFKPTLIVQQCGADSLGHDRLGCFNLNIKAHGECVKFVKSFGLPMLVVGGGGYTPR
                                                                                                                                                                               KVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTIR
                                                                                                                                                                                                                             YTTDRVFTLSFHKYNGEFFPGTGDLTEIGCDKGKHFALNVPLEDGIDDDSYINLFKSIVD
                                                                                                                                                                                                                                                                                                               QSDIAINWSGGLHHAKKNSPSGFCYVNDIVLSILNLLRYHPRILYIDIDLHHGDGVQEAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.4%; Score 1003.5; DB 2;
44.0%; Pred. No. 4.8e-72;
tive 86; Mismatches 127;
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                                      hypothetical protein YPR068c - yeast (Saccharomyces N;Alternate names: hypothetical protein YP9499.23c C:Species: Saccharomyces cerevisiae C:Date: 08-Jul-1995 *Sequence_revision 19-Oct-1995 *C:Accession: S54089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Gene: acuCl
A:Gene: acuCl
C:Superfamily: acetylpolyamine aminohydrolase;
F:6-306/Domain: RPD3/acuC homology <RAH1>
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C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
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A;Accession: D70388
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  R;Badcock, K.; submitted to t
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A; Residues: 1-375 <AQF>
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Best Local S
Matches 127
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nes 127; Conserv
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the EMBL Data Library,
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                      Churcher, C.
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A;Reference number: S54059
A;Accession: S54089
A;Nolecule type: DNA
A;Residues: 1-470 <BAD>
A;Residues: 1-470 <BAD>
A;Cross-references: EMBL:249219; NID:9805025; PID:9805048; MIPS:YPR068c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: SGD:HOS1
A;Gene: SGD:HOS1
A;Gross-references: SGD:S0006272; MIPS:YPR068c
A;Map position: 16R
C;Superfamily: RPD3/acuC homology <RAH1>
Search completed: April 26, 2002, 17:52:47 Job time: 110 sec
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Best Local Similarity
Matches 104; Conservat
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                                                                                                          377 LLMSRFYTYLT 387
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                                                                                                                                                                                                                                                                             260 YSKQIQTISVHLYEPGFFPGTGSLSDSRKDKN---VVNIPLKHGCDDNYLELIASKIVNP 316
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                                                                                                                                                  318 RNVARCWCYET 328
                                                                                                                                                                                                                              260 VMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHAD-CLRFLRSY-NVPLMVLGGEGYTI 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 ESMGDP------ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 PMKPH-RIRMAHSLIIHYHLHRRL-EISRPSLADASDIGRFHSPEYVDFLAS-----VSP 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.1%; Score 436; DB 2; Length 470; ilarity 28.0%; Pred. No. 6.8e-27; Conservative 67; Mismatches 116; Indels
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2544
1 MEADESGISLPSGPDGRKRR.....TGEDEMDDDNPEPDYNPPSS
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PGTUS_COMB.pep:*
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US-09-282-305-6
US-09-282-305-6
US-08-717-365-1
US-08-717-365-1
US-09-282-305-4
US-09-2446-504-80
US-09-446-517-2
US-08-291-896-2
US-08-867-611-2
PCT-US-29-6865-7
US-08-291-896-2
US-08-485-78-2
US-09-286-691-15
US-09-286-691-15
US-09-286-691-15
US-09-366-917-5
US-08-486-091-105
US-08-486-091-105
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US-08-486-097-105
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495.746 Million cell updates/sec
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2305  tone Deacetylases And Their Uses 709/282,305 31 080,563  Score 1734; DB 4; Length 458; Pred. No. 1.5e-183;	One Deacetylases And Their Uses  O9/282,305 1 1	One Deacetylases And Their Uses  Op/282,305  1  80,563  Score 1734; DB 4; Length 458; pred. No. 1.5e-183; Indels 22; Gaps; Mismatches 73; Indels 22; Gaps; Mismatches 74; Indels 22; Gaps; Mismatches 75; Indels 22; Indels 22

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297 CLRFLRSYNVPMMVLGGGGYTTRNVARCWCYETAVAVGVEPDNKLPYNDYYEYFGPDYTL 356

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RESULT 3
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US-09-282-305-8
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TYPE: PRT
ORGANISM: Zea mays
US-09-282-305-8
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Best L
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Patent No. 6287843
Sequence 6, Application
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CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
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                                                                                  420
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKR 181
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                                                                                                               SGTATYESDSDDDD 433
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                                                                                                                                                                                                                 SFNVPLLLLGGGGGYTIRNVARCWCYETGVALGQEPEDKMPVNEYYEYFGPDYTLHVAPSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OVYRPNPARDRDLCRFHADDYINFLRSVTPETQQD--QIRLLKRFNVGEDCPVFDGLYSF 123
                                                                                  -----DSDMEVDD
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Pred. No. 3.2e-163;
9; Mismatches 72;
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Patent No. 6287843
GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histo
FILE REFERENCE: 5718-44,
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                                                                                                                                                                                    Sequence 1, Application US/08528255A Patent No. 5659016 GENERAL INFORMATION:
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Best Local :
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PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
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                                                                                                                      APPLICANT: NAKAMURA, YUSUKE APPLICANT: FURUKAWA, YOIGTITLE OF INVENTION: RPDL PROTITLE OF INVENTION: ENCODING
                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                    NUMBER OF SEQUENCES:
STREET: 2026 Rami
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKR 181
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                                                                                                                                                                                                                                                                                                                ---HDADSDVEMNDAKPL 430
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                                                   2026 Rambling
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                                                                                                                    FURUKAWA, YOICHI
NTION: RPDL PROTEIN
NTION: ENCODING THE
                                                                       FLYNN,
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                                                                     THIEL, BOUTELL & TANIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/080,563
                                                     Road
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
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LIBRARY: human
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NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32549
REFERRNCE/DOCKET NUMBER: FV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC/XT/AT COMPAT
OPERATING SYSTEM: MS-DOS 5.0
SOTWARE: WORDPEFFECT 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                       316 TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR 375
                                                                                                                                                                                                                                                                                                                      256 LIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGY 315
405 I ---- SICSSDKRIACEEEFSDSEEE 426
                                            436 LHGYSCRGGATTDRDSTGEDEMDDDNPE 463
                                                                                             364 QRLFENLRMLPHAPGVQMQAIPE-DAIPEESGDE--
                                                                                                                                                                                          304 TIRNVARCRTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIK 363
                                                                                                                                                                                                                                                                                          244 VMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGY 303
                                                                                                                                                                                                                                                                                                                                                                                          184 EEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 LNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 KYHSDDYIKFLRSIRPDNMSEYS--KQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 GRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIG 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMT 65
                                                                                                                                           NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP 435
                                                                                                                                                                                                                                                                                                                                                                                                                    EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP 255
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US-08-717-365-1
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Patent No. 5763182
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: FURUKAWA, YOYO
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                       Matches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/717,36
FILING DATE: 23-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/528 255
FILING DATE: September 14, 1995
APPLICATION NUMBER: 196-227896
APPLICATION NUMBER: 196-227896
PILING DATE: 22-SEPTEMBER: 1994
APPLICATION NUMBER: JP7-183763
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INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32549
REFERENCE/DOCKET NUMBER: FU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
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                                                                            124
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     184
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CITY: Kalamazoo
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                                                                                                                                                                        76 REHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135
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EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP 255
                                                                          LNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV 183
                                                                                                             LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV 195
                                                                                                                                                  KYHSDDYIKFLRSIRPDNMSEYS--KQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVK 123
                                                                                                                                                                                                                             GTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAFEMT 65
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                                                                                                                                                                                                                                                                                                                     56.9%; Score 1448.5; 58.3%; Pred. No. 7.6;
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                                                                                                                                                                                                                                                                                                   79;
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                                                                                                                                                                                                                                                                                                                       .6e-152;
                                                                                                                                                                                                                                                                                                                                        DB 1;
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; SEQ ID NO 4
; LENGTH: 351
; TYPE: PRT
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US-09-282-305-4
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US-09-282-305-4
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Best Local S
Matches 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 I ----- SICSSDKRIACEEEFSDSEEE 426
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                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 LHGYSCRGGATTDRDSTGEDEMDDDNPE
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                                          358 DPSPMENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRP--K 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEADESGISLPS----GPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHL 57
QPKSVENLNTTKDLENIKNMILENLSKIEHVPSTQFHDRPSDPEAPEEKEEDMDKRPPQR 311
                                                                                                          RFLRSYNVPLAVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAASGEGASLPSPAGGEDAHRRRVSYFYEPSIGDYYYGQGHPMKP------45
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                                                                                                                                                                           VPLSDGIDDTTFRGLFQCIIKKVMEVYQPDVVVLQCGADSLAGDRLGCFNLSVKGHADCL
                                                                                                                                                                                                                   VPLNDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCL 297
                                                                                                                                                                                                                                                             FHRRVLYVDIDVHHGDGVEEAFFTTNRVMTVSFHKYGDFFPGTGHITDVGAAEGKHYALN 131
                                                                                                                                                                                                                                                                                                                                                                                            LFDFCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLK 177
                                                                                      RFLRSYNVPMMVLGGGGTTIRNVARCWCYETAVAVGVEPDNKLPYNDYYEYFGPDYTLHI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HERLEISRPSLADASDIGREHSPEYVDFLASVSPESMGDPSAARNLRRENVGEDCPVFDG 117
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Matches
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases
FILE REFERENCE: 5718-44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SED ID NOS: 18
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          68 ADYVEFLHRITPDS--QHLYASELTRYNLGEDCPVFDNLFEFCQIYAGGTLDAARRLNHK 125
                                                                                                        LEQLSGL1HAPSYQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTAT-----YESDS
                                                                                                                                                                           NVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIRNTL
                                                                                                                                                                                                                     KVVETYLPGAIVLQCGADSLARDRLGCFNLSIEGHAECVKFVKKFNIPLLVTGGGGYTKE
                                                                                                                                                                                                                                                                                                                                                                DADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVFEAF 199
                                    DDD 432
                                                                        MESLRYIQHAPGVQMQEVPPDFYIPDFDEDELD--PDERVDQHTQDKQIHRDDEYYEGDN
                                                                                                                                              NVARCWAVETGYLLDTELPNEIPKNEYIEYFAPDYTLKVPNLNMDNLNSKTYLSSIKVQV
                                                                                                                                                                                                                                                         KVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTIR
                                                                                                                                                                                                                                                                                             YFTDRVMTVSFHKYGDLFFPGTGDIKDIGEREGKYYAINIPLKDGIDDTSFTRPFKTIIA
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55.6%; Pred. No. 7.5e
tive 64; Mismatches
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ches 107;
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US-09-446-504-80

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Sequence 80, Applicat patent No. 6218150 GENERAL INFORMATION:

Application US/09446504

APPLICANT:
APPLICANT:

UEMORI, Takashi SATO, Yoshimi

TYPE: PRT

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US-09-144-085-2

Sequence 2, Application US/09144085

Patent No. 6280999

GENERAL INFORMATION:
APPLICANT: Gustafsson, Claes
APPLICANT: Betlach, Mary C.
APPLICANT: Ashley, Gary
APPLICANT: Julien, Bryan
APPLICANT: Ziermann, Rainer
ITILE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND
ITILE OF INVENTION: THEREFOR
ITILE OF INVENTION: THEREFOR
CURRENT APPLICATION NUMBER: US/09/144,085

CURRENT APPLICATION NUMBER: US/09/144,085
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CURRENT APPLICATION NUMBER: US/09/446,504
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
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LENGTH: 335
EARLIER APPLICATION NUMBER: 09/010,809
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
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Best Local Similarity
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APPLICANT:
APPLICANT:
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SOFTWARE: Patentin Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDYIYVWDEIVLPIVEEVKPKVIVISAGFDGFKGDGLTTLRLTESFYSYAGATLNKYPLA 28:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVP 306
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MUKAI, Hiroyuki
ASADA, Kiyozo
KATO, Ikunoshin
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                                                                                                                                                                                                             AND ENCODING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                   TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1466 GLEAPG------ARELVQSLEELGAETVTVAACDVSKREEVARVLAGIDAARPLS 1514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLESSGELPALFRALLRPSLRKASSATRRDASALRERLSALPEAERLNALVELVRGEVAA 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMDDES----FRSLFRPLIQKVMEVYQPEAVVLQCGADSL-SGDRLGCFNLSVKGHADC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKPLHGYSCRGGATTD 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLND 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGQSNYAAANTFLDALAAHRRGGGL--AATSLAWGFWTQAGVGMTAHLGEAELSRM-RRN 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVKLNRQ-----DADIAINWGGGLHHAKKSEASGFCYVNDI----VLGILELLKMFKRV 182
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                                   4150
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20.1%; Pred. No. 0.68;
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OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2
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Patent No. 5691306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                      NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,362
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
SEQUENCE
                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Deehr, Manya S.
REGISTRATION NUMBER: 37,120
REFERENCE/DOCKET NUMBER: 691
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING TITLE OF INVENTION: PROTEIN PRODUCTION
                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Dav
APPLICANT: Wada, Ikuo
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                   TELEFAX: (20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     823 VRFGDGIRALGKLGTGSFLEVGPDGVLTAMARACVTAAPEPGHRGEQGADADAHTALLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 GATTDRD ---- STGED 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             981 RAERIDPDRA-----FRDLG------FDSLTALELRDRLDTAL-----GLRLPS 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               941 HPRPADDTESG. TGRTEASPPRPHDVLHLVRSH--AAAVLG------HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 883 ALRRGRDEA··RSLTEAVARLHLHGVPMDWTSVLGGDVSRVPLPTYAFQRESHWLPSGEA 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 VHHGDGVEE-----AFYTT--DRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 76; Conserv
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 C
                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVQFQHTPP--VNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKPLH--GYSCR--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIRNTLLEQLSGLIHAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVLFDHPSPGALARFL---QGDDTRRPEPGKTNGTRATEPGPDPDDEPIAIVGMACRFPG 1075
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  CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6300 Columbia Center, 701 Fifth Avenue
                                                             (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas, David Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEED and BERRY
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                                                                                                                           690066.401C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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; MOLECULE TYPE: protein
US-08-296-362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-867-611-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08867611 Patent No. 6172189
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                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DAWSON, GEORGE J
APPLICANT: GUTIERREZ, ROBIN A
APPLICANT: LESNIEWSKI, RICHARD R
APPLICANT: STEWART, JAMES L
APPLICANT: RUPPRECHT, KEVIN R
APPLICANT: RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 FGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 YEEKHAKRPDADLKTYFTDKKTHLYTLILNPDNSFEILVDQ--SIVNSGNLLNDMTPPVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 VAVGVE------PD-----NKLPYNEYF--EYFGPDYTLHV---DPSPMENI 365
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                                                                                                                                                                                                                                                                                                                       STREET: ONE ABBOTT CITY: ABBOTT PARK
                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1997
                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 FADSF-----IAKYDGKWEVDE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
APPLICATION NUMBER:
                    FILING DATE:
                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TORDSTGEDEMDDDNPE----PDVNPP 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQNGIECGGAYVKLLSKTPELNLDQFHDKTPYTIMFGPDKCGEDYKLHFIFRHKNPKTGV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70;
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                                                                                                                                                                                                                                                                                                                                                ONE ABBOTT PARK ROAD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAILEY, STEPHEN H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASEY, JAMES M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESAI, SURESH
                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVARE, SUSHIL G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.7%; Score 93; DB 1; Length 593; 21.4%; Pred. No. 0.26;
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                                                                                                                         US/08/867,611
US/08/179,896
                                         US/08/646,757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --IRN-----TLLEQLSGLIHAPSVQFQHTPPVN 400
                                                                                                                                                                                                                                                                                                                                                   CHAD377/AP6D2
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: US 07/614,069

FILING DATE:

07-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07 FILING DATE: 24-AUG-1990

US 07/572,822

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                                                                                                                                                                                                                                                                                                       PCT-US92-06965A-7
                                                                                                                                                                                                                                                          Sequence 7, Application PC/TUS9206965A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.6%;
Best Local Similarity 22.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                   APPLICANT: DEVARE, S.
APPLICANT: DESAI, S.
APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
TITLE OF INVENTION: HCV SYNTHETIC PEPTIDE FROM NS1 REGION
NUMBER OF SEQUENCES: 35
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
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                           STREET: ONE ABBOTT PARK ROAD CITY: ABBOTT PARK
STATE: ILLINOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 -- NPNAVKVVLDAEGYAL-----YFSRATIPWDRDR---FAEGLETVGDNFLRHLGI 184
                                                                                                                                                                                                                                                                                                                                                                                           234 -- VDTPEDLDPSTNSMSTNPKPQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                  401 RVLDEPED-----DMETRPKPR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 LRSYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHV-- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 LNDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRF 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 YGYRAGFIRRYVNWQPSPLEHIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 GYEEAFYTTDR------VMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 VNVQCDE-----PMI-----PATIIRQV-ADNLAQRQVGMATLAVPIHNAEEAF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 GAERIIVATDHEDVARAVEAAGGEVCMTRADHQ-----SGTERLAEV-VEKCAFSDDTVI 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: POREMBSKI, PRISCILLA E REGISTRATION NUMBER: 33,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/748,561 FILING DATE: 21-AUG-1991
                  COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
60065-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 4; Length 396; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MLEQLRVLWYGEKIHVAVAQEVPGTG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Indels 88; Caps
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RESULT 14
US-08-291-896-2
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Best Local Similarity 22.*
Witches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08291896 Patent No. 5480800
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 820 amino acids
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: NITE OF THE CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PCT/US92/06965A
                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 708-937-6365
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 RVLDEPED-----DMETRPKPR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 GVEEAFYTTDR-------VMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVP 239
                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Palaman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 -- VDTPEDLDPSTNSMSTNPKPQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 LRSYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 YGYRAGFIRRYVNWQPSPLEHIE----
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                                                                                 APPLICATION NUMBER: US/08/291,896 FILING DATE: 17-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                            PatentIn Release #1.0,
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22.4%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                DNA fragment carrying the gene encoding the enzyme for fragmenting N-acetylheparosan and the adjacent sequences permitting its expression, recombinant enzyme intended for fragmenting N-acetylheparosan and its use.
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                                                                                                                                               Version
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,278
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Legoux, Richard
APPLICANT: Leiong, Philippe
APPLICANT: Leiong, Philippe
APPLICANT: Salome, Marc Louis Victor
TITLE OF INVENTION: DNA fragment carrying the gene encoding the enzyme for
TITLE OF INVENTION: fragmenting N-acetylheparosan and the adjacent sequences permititle OF INVENTION: recombinant enzyme intended for fragmenting N-acetylheparosan
                                                                                                                 FILING DATE: 17-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9:
FILING DATE: 17-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                             FILING DATE: 17-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 DEPEDDMETRPKPRX---WSGTATYESD-----SDDDDKPLHGYSCRG 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 YVDAAIAGVIGGFGWF------IQYGSG---AVYRT-----FQDKMRDGVSI 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
ZIP: 200
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                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 400 Seventh S CITY: Washington D.C.
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STRANDEDNESS: sir
TOPOLOGY: linear
                   NAME: Player, William E. REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                        CLASSIFICATION: 435
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                    US 08/291,896
                                                                                                                                                                                            FR 93/10050
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TOPOLOGY: 1:
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Best Local Similarity
Matches 69; Conserv
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TELEPHONE: (202) 638-666
TELEFAX: (202) 393-5950
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                          404
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                                                                                                                                                                                                                                                                                            277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                        DEPEDDMETRPKPRX---WSGTATYESD----SDDDDKPLHGYSCRG 443
                                                                                                                          DYTLHVDPSPMEN-----LNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVL 403
                                                                                                                                                                    SGGHDVSVKNIRFTNTRGPGFSLIAYPDNGIPSGYIVRDIRGEYLGFANNKKAGCVLFDS
                                                                                                                                                                                                                                                      GTGGGTIKQYDRDGNHLVFNMPDGGMLSTLTIMGNKSDDSVQGH------QVSF 295
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                                                                                                                                                                                                            LGGEGYT I RNVARCWCYETAVAVGVEPDNKLP-----YNEYFEY-----FGP
                                                                                                                                                                                                                                                                                            SLSG-----SVKGHADCLRFLRSYNVPLMV
SSV---MANNPKYAAVVVGKGTGNLISDVLVDYSESDAKQAHGVTVQG
                                                                                SQNTLIDGVIARNYPQFGAVELKTAAKYNIVSNVIGEECQHVVYNGTE--TETAPTNNII 413
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Search completed: April 26,
Job time: 35 sec 2002, 17:51:27

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Arabidopsis Arabidopsis

## ALIGNMENTS

RESULT AAB67812

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AAB67812;

AAB67812 standard;

Protein;

471

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elongation), comprises Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocoty) Miki B, CA2316036-A1 Arabidopsis thaliana Histone deacetylase; AtRPD3B; RPD3; gene expression; transgenic plant; Amino acid sequence of a histone deacetylase designated AtRPD3B 29-JUN-2001 (first entry) N-PSDB; 27-AUG-1999; 24-AUG-2000; 2000CA-2316036. 27-FEB-2001. HDA1; ethylene-responsive phenotype; (MIAC ) 2001-258457/27. DB; AAF80351. CANADA MIN AGRIC & AGRI-FOOD CANADA Brown D, Tian L, 99US-0383971. introducing genes encoding histone deacetylase Š <u>.</u> hypocotyl elongation

Result

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Score

Match

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Description

SUMMARIES

AAB67812 AAG05187 AAG39372

Query

2542 2535 2535 2318 2318 2379 2279 2279 2279 1561.5 1561.5

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    Arabidopsis thaliana
                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 1499.
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                              termination sequence
                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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01-APR-1999;

06-APR-1999;

08-APR-1999;
 18-JUN

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9US-0140	8-JUN-199	PR	quence.	
90S-0140	4 - JUN - 199	PR	hybridisation assay; genetic mapping; gene expression control; promoter;	
908-0140	3 - JUN - 199	מי מ	figstion: olars transduction pathway, motabolic	
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Length 425;

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Best Local Similarity
                                                                                                                                                                                                                                                              Maize histone deacetylase; HD; HD cDNA; family 1, ZmHD1; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                              N-PSDB;
                                                                                                                                                                                                                                                      disease response
                                                                                                                                                                                                                                                                                                                                     13-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    AAY28797 standard; protein; 458
           New deacetylase genes, used for producing transgenic plants which increased disease resistance -
                                              WPI; 1999-611038/52
N-PSDB; AAX90837.
                                                                                 Baldwin DA,
                                                                                                                                 03-APR-1998;
                                                                                                                                                        02-APR-1999;
                                                                                                                                                                                14-OCT-1999
                                                                                                                                                                                                       WO9951731-A2
                                                                                                                                                                                                                                                                                                               Maize histone deacetylase-1.
                                                                                                        (PION-) PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPPSS 471
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                                                                               Briggs
                                                                                                                                9805-0080563
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Pred. No. 7.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is maize histone deacetylase encoded by HD cDNA belonging to family 1, ZmHDJ. This enzyme responsible for removing acetyl modifications, may be localised to promoters targeted for repression by other proteins that associate with HD and specifically bind regulatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transgenic plants with increased disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
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                24-AUG-2000; 2000CA-2316036
                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                          Histone deacetylase; AtRPD3A; RPD3; gene expression; transgenic plant;
                                                                                                                                                                                                                                                                                                                    AAB67811 standard; Protein;
                                                   27-FEB-2001
                                                                                    CA2316036-A1
                                                                                                                                                        HDA1; ethylene-responsive phenotype; hypocotyl elongation
                                                                                                                                                                                                           Amino acid sequence of a histone deacetylase designated AtRPD3A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               designated AtrPDJA. The protein is homologous to yeast RPDJ and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative ensociation with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant, particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                              ----dmdvdddrkpipsrvkreavepdtkdkdglkgimergkgcevevdesgstkvtgvn
                                                                         TATYESDSDDDDKP--
                                                                                                                                         ASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVL 183
                                                                                                                                                                                                                                                                                                                                                           nknsrqmleeirndllhnlsklqhapsvpfqerppdtetpevdedqedgdkrwdpds---
                                                                                                             NUTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRV--LDEPEDDMETRPKPRXWSG
                                                                                                                                                                     NVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPME 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents Arabidopsis thaliana histone deacetylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.4%; Score 1561.5; DB 2 60.7%; Pred. No. 5.8e-158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Mismatches
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                                                                        -LHGYSCRG-GATTDRDSTGEDEMDDDN
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The present invention describes a method of suppressing the expression a gene of interest by introducing into the cell a protein containing a DNA binding site and a chromatin inactivation portion, or a nucleotide encoding such a peptide. Preferably the chromatin inactivation portion part of the histone deacetylation (HDAC) complex. The method can be use in disease treatment, for example in the treatment of cancer by the suppression of oncogenes, and in the production of disease models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suppressing expression of selected gene for treating cancer, involves introducing peptide comprising nucleic acid binding portion that binds to or associated with selected gene and chromatin inactivation portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB67165 standard;
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99GB-0015126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease model; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                    65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       histone deace
DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deacetylation
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Local Similarity
                                                                                                             YIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDG
                                                                                                                                                                                                                       ASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVL
                                                                                                                                                                                                                                                                                       SRPSLADASDIGRFHSPEYYDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCR 123
                                                                                                                                                                             tyaggsvggsvklnhglcdiainwagglhhakkceasgfcyvndivlailellkqhervl
                                                                                                                                                                                                                                                                lkpfparerdlcrfhaddyvsflrsitpetqqd-~qirqlkrfnvgedcpvfdglysfcq
                                                                                                                                                                                                                                                                                                                                                    dtggnslasgpdgvkrkvcyfydpevgnyyygqghpmkphrirmthallahygllqhmqv 61
                                                                                                                                                                                                                                                                                                                                                                                                DESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEI 63
iddesyhllfkpimgkvmeifrpgavvlqcgadslsgdrlgcfnlsikghaecvkfmrsf
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.4%;
60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1561.5;
Pred. No. 5.8e:
64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           .8e-158;
les 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 501;
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RESULT 11
AAY58829
ID AAY588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
               Query Match
Best Local Similarity
 Matches 290;
                                                                                                                                                         plant histone deacetylases. The invention relates to isolated rice, soybean and wheat nucleic acid fragments encoding HDL. It also relates to the construction of a chimeric gene encoding all a portion of HDL, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HDL in a transformed host cell. The availability of
                                                                                                              nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in eukaryotic cells, and will also provide mechanisms
                                                                        Sequence
                                                                                                    control transcriptional gene regulation in plants
                                                                                                                                                                                                                                                 (HD1), a chromatin associated protein, as deduced from a soybean root cDNA clone (see AAZ58260) isolated on the basis of homology \,
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ58260
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-182439/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 · JUL · 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200004177-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soybean; transgenic plant; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromatin associated protein; histone deacetylase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soybean histone deacetylase 1 (HD1) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY58829 standard; Protein; 473
                                                                                                                                                                                                                                                                              The present sequence is that of soybean histone deacetylase I
                                                                                                                                                                                                                                                                                                                                       transforming plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 p 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 ----dmdvdddrkpipsrvkreavepdtkdkdglkgimergkgcevevdesgstkvtgvn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364
                                                                                                                                                                                                                                                                                                                                                     nucleic acid fragment useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATYESDSDDDDKP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRV--LDEPEDDMETRPKPRXWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt nvpllllggggytirnvarcwcyetgvalgvevedkmpeheyyeyfgpdytlhvapsnme}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPME 363
                                                                                                                                                                                                                                                                                                                                                                                                                              RE,
                                                                                                                                                                                                                                                                                                            Page 27-28;
                                                                          473 AA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Vollmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0092841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US15807
               61.3%; Score 1558.5; DB 21; Length 473; 61.8%; Pred. No. 1.1e-157;
                                                                                                                                                                                                                                                                                                           36pp; English.
 71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LHGYSCRG-GATTDRDSTGEDEMDDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ħ
                                                                                                                                                                                                                                                                                                                                                       probes and primers,
 83;
 Indels
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 Gaps
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RESULT 1
AAY28800
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                                                                                                                                                                                                                                                                                                                      Maize histone deacetylase; HD; HD cDNA; family 1, ZmHD1; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                            Claim
                                                                                                                                                                                                                 02-APR-1999;
                                                                                                                                                                                                                                                                W09951731-A2
                                                                                                                                                                                                                                                                                                             disease response promoter.
                                                                                                                                                                                                                                                                                                                                                                       Maize histone deacetylase-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY28800 standard;
                                                                  New deacetylase genes, used for producing transgenic increased disease resistance
                                                                                                       N-PSDB; AAX90840
                                                                                                                   WPI; 1999-611038/52
                                                                                                                                         Baldwin DA, Briggs
                                                                                                                                                                 (PION-) PIONEER HI-BRED
                                                                                                                                                                                                                                        14-OCT-1999.
                                                                                                                                                                                                                                                                                        Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nknsrqlldeiraklldnlsrlqhapsvpfqerppdaellerdedqddrder....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nvpllllggggytirnvarcwcfetsvalgielddkmpqheyyeyfgpdytlhvapsnme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASAGGS I GAAVKLNRQDAD LA INWGGGLHHAKKSEASGFCYVND I VLG I LELLIKMFKRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATYESDSD----DDDKPLH---GYSCRGGATTDRDS-TGEDEMDDDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iddesyqslfkpimgkvmeifrpgavvlgcgadslsgdrlgcfnlsikghaecvrymrsf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        esggnslpsgsdgvkrkvsyfydpevgnyyyggghpmkphrirmthallahygllqhmqv 61
                                          1; Page 63-65; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -wdpdsdrevgddsnpvrrrvksecvd--aedkdtvsgvdsmavdep 455
                                                                                                                                                                                         98US-0080563
                                                                                                                                                                                                                99WO-US07370
                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 517
                                                                                                                                          SP,
                                                                                                                                                                   TNI
                                                                                                                                          Crane VC:
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                                                                               plants which have
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belonging to family 1, ZmHD1. The modifications, may be localised

ZmHD1.

This enzyme responsible ed to promoters targeted

for

removing acetyl

The present sequence is maize histone deacetylase encoded by HD cDNA

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RESULT 13
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other proteins that associate with HD and specifically bind regulatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transgenic plants with increased disease resistance. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                                                                                   acetyl modification; promoter; regulatory element;
disease resistance; toxin screening; pathogenicity;
disease response promoter.
                                                                                                                                                                                                                                                                                                    13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                 AAY28799
                                                                                                                                                                                                                                      Maize histone deacetylase; HD;
(PION-) PIONEER HI-BRED INT INC
                                03-APR-1998;
                                                               02-APR-1999;
                                                                                                                             W09951731-A2
                                                                                                                                                         Zea mays
                                                                                                                                                                                                                                                                     Maize histone deacetylase-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vlyvdidihhgdgveeafyttdrvmtvsfhkfgdyfpgtgdirdighskgkyyslnvpld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cqtyagasvggavkln-hghdiainwsgglhhakkceasgfcyvndivlailellkhher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRASAGGSIGAAVKLNRODADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGTATYESDSDDDD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \textbf{menkntrqq} \\ \textbf{lddirsklldnlsklrhapsv} \\ \textbf{hfqervpdteipeqdedqddpderhdp---}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRV--LDEPEDDMETRPKPRXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sfnvpllllggggytirnvarcwcyetgvalgqepedkmpvneyyeyfgpdytlhvapsn
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                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                    (first entry)
                                98US-0080563
                                                               99WO-US07370
                                                                                                                                                                                                                                                                                                                                                              protein; 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1551.5; DB 20; Length 517; Pred. No. 7.2e-157;
                                                                                                                                                                                                                    HD cDNA; family 1, ZmHD1; gene repression;
regulatory element; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 58-60; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New deacetylase genes, used for producing transgenic plants which have increased disease resistance .
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                                                                                                                                         AAY58828 standard; Protein; 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qvfrphpardrdlcrfhaddyvsflrsvtpetqqd--qiralkrfnvgedcpvfdglysf 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDF 121
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                                                                                                                                                                                                                                                                                      menkntrhqlddiksklldnlsklrhapsvqfqerppeaelpeqded--kenpder----
                                                                                                                                                                                                                                                                                                                     MENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLR
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                                                                                                                                                                                                                        ---hdadsdvemndakpl 430
                                                                                                                                                                                                                                                                                                                                                 {\tt sfnvpllllggggytirnvarcwcyetgvalgheltdkmppneyyeyfgpdytlhvapsn}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.7%; score 1520; DB 20; 66.0%; Pred. No. 1.3e-153; tive 56; Mismatches 77;
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Chromatin associated protein; histone deacetylase rice; transgenic plant; transcription regulation.

gene

Rice histone deacetylase 1 (HD1) protein (C-terminal portion).

(first entry)

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO
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sklrhapsvqfqerpp-eaelpeqdedqed-pder---
                                                                                                                                                                                                                                                                                   vfrpg \verb"a" v Ligg a d s Lig d r Lig fine strong the strong strong through the strong strong
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                                                                       SGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSD---DDDKPLHGY 439
                                                                                                                                       CWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIRNTLLEQL
                                                                                                                                                                                                                                                                                                                                                               VYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTIRNVAR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEEAFYTT 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iainwagglhhakkceasgfcyvndivlailellkyhgrvlyvdidihhgdgveeafytt 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.9%; Score 1498; DB 21; 64.4%; Pred. No. 3.5e-151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55;
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Matches 262; Query Match Best Local Similarity

Conservative

79;

Mismatches

80;

Indels

27;

Gaps

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57.5%; Score 1462.5; DB 18; Length 482; 58.5%; Pred. No. 2.2e-147;

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                                                                                                                                                                                                              influencing cell cycle progression or to modulate gene transcription. The products can be used for diagnosis and therapy. They can be used, for example, to treat tumours or proliferative disorders or spermatogenesis, osteogenesis, chondrogenesis or the differentiation of progenitor cells. They can also be used to treat psoriasis, bone diseases, fibroproliferative disorders, degenerative disorders, or for repair of cartilage, increasing bone density, liver repair subsequent to a partial population, increasing bone density, liver repair subsequent to a partial population.
                                                        also be used in cell cultures.
note: in the claims, the full length HDl sequence is
referred to as SEQ. ID. No.2; from the disclosure it
                                                                                                                                     hepatectomy, to promote regeneration of lung tissue in the treatment of emphysema, or for inducing tolerance in autoimmune diseases, and transplant recipients. HDx inhibitors can be used as anti-fungal agents, preservatives in foodstuff, feed supplements for promoting weight gain i
                                                                                                                                                                                                                                                                                                                                                        polypeptide, designated HDI. The HDx polypeptides are capable of modulating proliferation survival and differentiation of cells. The proteins are able to alter chromatin structure by descetylating histones such as H3 or H4. They have the ability to modulate cell growth by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated histone deacetylase polypeptide(s) and genes - used develop products for modulating the proliferation, survival or differentiation of cells, e.g. for treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histone deacetylase gene; HDx; HDl; HDx polypeptide; deacetylation; H3 H4; cell differentiation; chromatin structure; cell cycle progression; proliferative disorder; fibroproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Pages 112-114; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A novel histone deacetylase (HDx) protein, designated HD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW29324 standard;
Sequence
                                                                                                                livestock, disinfectants, insecticides or defoliants. The products can
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a novel histone deacetylase (HDx)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degenerative disorder; autoimmune disease; HDx inhibitor
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                                     is SEQ. ID. No.5
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482 AA;
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	isicssdkriacepefsdseee 426	405	Db
	LHGYSCRGGATTDRDSTGEDEMDDDNPE 463	436	VΩ
404	grlfenlrmlphapgvgmgaipe-daipeesgdededdpdkr 404	364	Dр
435	NTLLEGLSGLIHAPSVQFQHTPPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP 435	376	Qy
363	tirnvarcwtyetavaldteipnelpyndyfeyfgpdfklhispsnmtngntneylekik	304	Db
375		316	Qy
303	vmskvmemfqpsavvlqcqsdslsqdrlqcfnltikghakcvefvksfnlpmlmlggggy 303	244	Ъ
315	LIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGY	256	QΥ
243	eeafyttdrvmtvsfhkygeyfpgtgdlrdigagkgkyyavnyplrdgiddesyeaifkp	184	Db
255	EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP	196	QY
183	lnkqqtdiavnwagglhhakkseasgfcyvndivlailellkyhqrvlyididihhgdgv 183	124	DЪ
195	LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV	136	Ϋ́
123	kyhsddyikflrsirpdnmseyskqmqrfnvgedcpvfdgifefcqlstggsvasavk	66	뫄
135	REHSPEYVDFLASVSPESMGDPSAARNLRRENVGEDCPVFDGLFDFCRASAGGSIGAAVK 135	76	QΥ
65	gtrrkvcyyydgdvgnyyyggghpmkphrirmthnlllnyglyrkmeiyrphkanaeemt 65	6	В
75		16	QY

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